

DR WPI: 2001-316417/33.
DR N-PSDB: AAH20574.
XX
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
PT syndrome and tumors, also related proteins and antibodies -
XX
PS Claim 10; Fig 4; 46pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding the MTR1
CC protein that: (i) has at least one biological activity of a TRP
CC (transient receptor potential) family protein; (ii) is connected with
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving 11p15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MTR1 is involved in
CC regulation of intracellular calcium ion levels, which are essential for
CC cellular responses to hormones and/or growth factors; also in apoptosis
CC and cell growth, death and differentiation, and in uterine diseases,
CC including polycystic kidney disease. (I) and related ribozymes, antisense
CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
CC associated with altered expression of the MTR1 gene or activity of its
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC thaboid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC used for diagnosis of such diseases. (I) can also be used for recombinant
CC production of MTR1 proteins (II) (used for analysis, characterization and
CC therapy), as tissue or chromosomal markers, for identifying genetic
CC diseases and related sequences, as primers for genetic fingerprinting, as
CC source of oligonucleotides for biochips, and to raise anti-protein or
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC competitive assays for (II), as tissue markers, for identifying
CC interacting proteins and in screening for (anti)agonists. This sequence
CC represents a human MTR1 protein described in the method of the invention.
CC
XX
SQ Sequence 1165 Aa;

Query Match 99.7%; Score 6073; DB 22; Length 1165;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MODVGGPRGPGDADREELGLHGEVNFSGGKRGKRVVPSGAVSVFDLLAMW 60
DB 1 MODVGGPRGPGDADREELGLHGEVNFSGGKRGKRVVPSGAVSVFDLLAMW 60
QY 61 HLPAPLVVSLVGEBOFPAMKSMRLDVKRGLVKAASGTGAMILTSALRGLARHVGQAV 120
DB 61 HLPAPLVVSLVGEBOFPAMKSMRLDVKRGLVKAASGTGAMILTSALRGLARHVGQAV 120
QY 121 RHSLASTSTKRVVAVAGASLGRVLRHRIEBAOEPFVHYPEDDGSQGPLCISLDSNL 180
DB 121 RHSLASTSTKRVVAVAGASLGRVLRHRIEBAOEPFVHYPEDDGSQGPLCISLDSNL 180
QY 181 SHPILVEPPPGKDGTLRLRLKHSIQRAGVGTSTIEIPVCLLVNDGPNTLERI 240
DB 181 SHPILVEPPPGKDGTLRLRLKHSIQRAGVGTSTIEIPVCLLVNDGPNTLERI 240
QY 241 SRAVEQAAMWLIVSGSGIADVLALVNOPHLIVPVAEKOFKPKSFMSIEDIVMT 300
DB 241 SRAVEQAAMWLIVSGSGIADVLALVNOPHLIVPVAEKOFKPKSFMSIEDIVMT 300
QY 301 KLLQNTSHOHLITVDFEQQSGSEEDTVILKALVACSHSQSEODYDELKLAAMDR 360
DB 301 KLLQNTSHOHLITVDFEQQSGSEEDTVILKALVACSHSQSEODYDELKLAAMDR 360
QY 361 VDIASEIFNGDVEMKSCLEVMVDALVSNKPEFRLVNDGADVADFLTGRLOELR 420
DB 361 VDIASEIFNGDVEMKSCLEVMVDALVSNKPEFRLVNDGADVADFLTGRLOELR 420
QY 421 SVSRKSLFDLLORKEEARLTLAGLGTQOAREPPAPPAFSLHEYSRLXDFLODACRG 480
DB 421 SVSRKSLFDLLORKEEARLTLAGLGTQOAREPPAPPAFSLHEYSRLXDFLODACRG 480
QY 481 FYODGPGGRRRAEKGPAPKPTGQKWLIDLNOKSENPMWDLFLMAVLQNRHEMATYFMAM 540
DB 481 FYODGPGGRRRAEKGPAPKPTGQKWLIDLNOKSENPMWDLFLMAVLQNRHEMATYFMAM 540

QY 541 GQGVAAALAAACKIKEMSHLETEAARATREAKYERLADLFSECSYSEARAFALLY 600
DB 541 GQGVAAALAAACKIKEMSHLETEAARATREAKYERLADLFSECSYSEARAFALLY 600
QY 601 RRNCWSKTTCLHATEADAKAFPAHDGVQAFTRIRWGMMACTPIRLIGALCFALV 660
DB 601 RRNCWSKTTCLHATEADAKAFPAHDGVQAFTRIRWGMMACTPIRLIGALCFALV 660
QY 661 YTNLITSEEPALRTGLEDLODLSLDEKSPVLGLOSRYEELVAPPAQDGRPAVFL 720
DB 661 YTNLITSEEPALRTGLEDLODLSLDEKSPVLGLOSRYEELVAPPAQDGRPAVFL 720
QY 721 LTRNRKFGAVTVFLGVVWYFAFLFTVYLLVDFEPPPGSGSEVTLFYWFVTLVL 780
DB 721 LTRNRKFGAVTVFLGVVWYFAFLFTVYLLVDFEPPPGSGSEVTLFYWFVTLVL 780
QY 781 EIRIQGFPTDDBTHLVKKFTLVYGDNNKCDMAIPLFIVGTCRMLPSAFAGRTVLAM 840
DB 781 EIRIQGFPTDDBTHLVKKFTLVYGDNNKCDMAIPLFIVGTCRMLPSAFAGRTVLAM 840
QY 841 DEWFTTLRLHIFAIHQKQGRKIIIVBERMKDVEFFELFSLVWLVAAGVTTQALLPHDG 900
DB 841 DEWFTTLRLHIFAIHQKQGRKIIIVBERMKDVEFFELFSLVWLVAAGVTTQALLPHDG 900
QY 901 RLEWIFRRVLRPYLQIFGQIPLDEIDBARVNCSTHPLLEDSPCSPSLVANMLVILLY 960
DB 901 RLEWIFRRVLRPYLQIFGQIPLDEIDBARVNCSTHPLLEDSPCSPSLVANMLVILLY 960
QY 961 TFLVTVNLVNLMIAMSYTFQVQGNATYFMKQRYNLIVEHERPALAPPLLSHL 1020
DB 961 TFLVTVNLVNLMIAMSYTFQVQGNATYFMKQRYNLIVEHERPALAPPLLSHL 1020
QY 1021 SLTLRRVKEAHEKREHLERDLPDLOKXVTEVTKENFLSMKERRRDSSEGVLRX 1080
DB 1021 SLTLRRVKEAHEKREHLERDLPDLOKXVTEVTKENFLSMKERRRDSSEGVLRX 1080
QY 1081 TAHRYDFIAKYLGLREOEKRIKCLSQINYSVLSVADVLAAQGGPRSSOHGEGESQ 1140
DB 1081 TAHRYDFIAKYLGLREOEKRIKCLSQINYSVLSVADVLAAQGGPRSSOHGEGESQ 1140
QY 1141 LVAADHRRGIDGWEQPGAGOPPST 1165
DB 1141 LVAADHRRGIDGWEQPGAGOPPST 1165

RESULT 2
ABB83855
ID ABB83855 standard; Protein; 1165 Aa.
XX
AC ABB83855;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human ltrpc6 SEQ ID NO 8.
XX
KW Human; ltrpc6; taste; cell signalling; TC-1CS; food; pharmaceutical;
KW taste cell-specific ion channel subunit.
XX
OS Homo sapiens.
XX
PN WO200254069-A1.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US49808.
XX
PR 29-DEC-2000; 2000US-259379P.
XX
PR 21-DEC-2001; 2001US-0026188.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zuker CS, Zhang Y;

Not available?

Shen

XX WPI: 2002-583632/62.
 DR N-PSDB: ABN85736.
 PT Identifying modulators of taste signaling in taste cells for use in
 PT food and pharmaceutical industries to customize and regulate taste, by
 PT determining effect of the compound on a taste cell-specific ion channel
 PT subunit
 XX
 PS Claim 1; Page 305; 306pp; English.
 CC The invention relates to identifying (M1) a compound that modulates taste
 CC signaling in taste cells, by contacting the compound with a eukaryotic
 CC host cell or cell membrane which expresses a taste cell-specific ion
 CC channel subunit (TC-ICS), and determining a functional effect of the
 CC compound upon a transmembrane ion flux of a predetermined ion.
 CC Identifying a compound that modulates taste signaling in taste cells.
 CC (M1) is useful for identifying a compound that modulates taste signaling
 CC in taste cells, for identifying a compound that binds to a taste cell
 CC specific ion channel subunit and for modulating taste signaling in taste
 CC cells of a mammal, in particular a human. Modulators identified by (M1)
 CC are used by the food and pharmaceutical industries to customize taste,
 CC e.g. as additives to food or medicine so that the food or medicine tastes
 CC different to the subject who ingests it. Bitter medicines can be made to
 CC taste less bitter and sweet substance can be enhanced. The modulators are
 CC useful for pharmacological and genetic modulation of taste signaling
 CC pathways. The taste modulators can be directly administered to mammalian
 CC subjects for modulation of taste in vivo. The present sequence is that of
 CC the predicted human ttrpc6 protein of the invention.
 CC
 XX Sequence 1165 AA;
 SQ
 Query Match 99.7%; Score 6073; DB 23; Length 1165;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLADLTFSECYNSSEARAFALLV 600
 QY RNRNCSKTTCLAHATEADAKAFPAHDVQAFRLIRIMGDMAGPILRLGAFICFALV 660
 DB 601 RNRNCSKTTCLAHATEADAKAFPAHDVQAFRLIRIMGDMAGPILRLGAFICFALV 660
 QY 661 RNRNCSKTTCLAHATEADAKAFPAHDVQAFRLIRIMGDMAGPILRLGAFICFALV 660
 DB 661 YTNLITFSEBAPLRTGLEDLDDLDLDTESKPLVGLQSRVELYAPPAQDGRPAVFL 720
 QY 721 YTNLITFSEBAPLRTGLEDLDDLDLDTESKPLVGLQSRVELYAPPAQDGRPAVFL 720
 DB 721 YTNLITFSEBAPLRTGLEDLDDLDLDTESKPLVGLQSRVELYAPPAQDGRPAVFL 720
 QY 721 LTRNRKFGAATVYFLGVNMYFAFLFTYVLLVDFRPPQSGSEPTVLYFWFTVLV 780
 DB 721 LTRNRKFGAATVYFLGVNMYFAFLFTYVLLVDFRPPQSGSEPTVLYFWFTVLV 780
 QY 781 BEIRQGFPTDDTHLVKFTLYVGDNNMKCMVAIFLIVGTORMLPSAEAGRTVLAM 840
 DB 781 BEIRQGFPTDDTHLVKFTLYVGDNNMKCMVAIFLIVGTORMLPSAEAGRTVLAM 840
 QY 841 DFMVFTLRLIHI PAIHKOLGPKIIVEREMKDVFFFLFSLVWLVAVGTTOALLHPHDG 900
 DB 841 DFMVFTLRLIHI PAIHKOLGPKIIVEREMKDVFFFLFSLVWLVAVGTTOALLHPHDG 900
 QY 901 RLEWIFRRVLYRPLYQIFGQIPLDEIDBARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
 DB 901 RLEWIFRRVLYRPLYQIFGQIPLDEIDBARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
 QY 961 TFLVLTNVLNMLLIAMSYTFQVQVGNATPMKFORNLIVYHERPALAPFLLSHL 1020
 DB 961 TFLVLTNVLNMLLIAMSYTFQVQVGNATPMKFORNLIVYHERPALAPFLLSHL 1020
 QY 1021 SLTLRRVPEKAEHREHLERDLDPDLQKVYTWETQKENFLSKMERGRDSEGEVLAK 1080
 DB 1021 SLTLRRVPEKAEHREHLERDLDPDLQKVYTWETQKENFLSKMERGRDSEGEVLAK 1080
 QY 1081 TAHAVDTIAKYLGLREGEKRIKCLSEQINYSVYSSVADVLAKGGPRSSQHGEGSQ 1140
 DB 1081 TAHAVDTIAKYLGLREGEKRIKCLSEQINYSVYSSVADVLAKGGPRSSQHGEGSQ 1140
 QY 1141 LVAADHGGIDCWEOPGAGCPSPDT 1165
 DB 1141 LVAADHGGIDCWEOPGAGCPSPDT 1165

RESULT 3
 ID AAM51708 standard; Protein, 1165 AA.
 XX AAM51708;
 AC AAM51708;
 DT 16-JAN-2002 (first entry)
 DE Human TRP8.
 KW Mouse; human; TRP8; transient receptor potential channel;
 KW taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
 KW pharmaceutical.
 OS Homo sapiens.
 PN WQ200179448-A2.
 PD 25-OCT-2001.
 PF 17-APR-2001; 2001WO-US12608.
 PR 17-APR-2000; 2000US-197491P.
 PR 13-APR-2001; 2001US-0834792.
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX Margolskee RF, Huang L, Rong M, Max M, Perez CA;
 PI

John's from 2/25

regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BMS, Wilms tumor, rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (II) can also be used for recombinant production of MTR1 proteins (II) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for bioclips, and to raise anti-protein or anti-DNA antibodies. (II) are used to raise Ab, as tissue markers, for competitive assays for (II), as tissue markers, for identifying interacting proteins and in screening for (ant)agonists. This sequence represents a human MTR1 protein described in the method of the invention.

Sequence 1179 AA;

Query Match 98.7%; Score 6014; DB 22; Length 1179;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1159; Conservative 1; Mismatches 4; Indels 16; Gaps 3;

1 MODVQPPSPGDAEDRRELGLHGEVNFSGSGKRGKRVPSGVA SVLFDLLAEW 60
1 MODVQPPSPGDAEDRRELGLHGEVNFSGSGKRGKRVPSGVA SVLFDLLAEW 60
61 HLPAPNVLVSLVGEOPAPKMSWLRDVLRKLVAAOAGTGMILTSALRVGLAHVQAV 120
61 HLPAPNVLVSLVGEOPAPKMSWLRDVLRKLVAAOAGTGMILTSALRVGLAHVQAV 120
61 HLPAPNVLVSLVGEOPAPKMSWLRDVLRKLVAAOAGTGMILTSALRVGLAHVQAV 120
121 RDHSLASTSTVYRVAVAGMAGSLGRVLRHRIIEAEOEDPVYPPEDGGSGPLSLDNL 180
121 RDHSLASTSTVYRVAVAGMAGSLGRVLRHRIIEAEOEDPVYPPEDGGSGPLSLDNL 180
121 RDHSLASTSTVYRVAVAGMAGSLGRVLRHRIIEAEOEDPVYPPEDGGSGPLSLDNL 180
181 SHFLVBERPGPKDGLTELRLLEKHISEQAGYGTGSIIEIPVLCILVNGDPTLERI 240
181 SHFLVBERPGPKDGLTELRLLEKHISEQAGYGTGSIIEIPVLCILVNGDPTLERI 240
181 SHFLVBERPGPKDGLTELRLLEKHISEQAGYGTGSIIEIPVLCILVNGDPTLERI 240
241 SRAVEOAAPMLILVSGGIAAVLALVNQPHLLVPKVAEKPKFKPKKPSMEDIVRWT 300
241 SRAVEOAAPMLILVSGGIAAVLALVNQPHLLVPKVAEKPKFKPKKPSMEDIVRWT 300
241 SRAVEOAAPMLILVSGGIAAVLALVNQPHLLVPKVAEKPKFKPKKPSMEDIVRWT 300
301 KLLONITSHOHLTVYDEPGSEELPTVILKALVKACKSHSOPDYLDELKLA VAWDR 360
301 KLLONITSHOHLTVYDEPGSEELPTVILKALVKACKSHSOPDYLDELKLA VAWDR 360
301 KLLONITSHOHLTVYDEPGSEELPTVILKALVKACKSHSOPDYLDELKLA VAWDR 360
361 VDIKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
361 VDIKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
361 VDIKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
421 SVSRKSLIFDLLOKQOEARLTLAGLGTQARREPPAPASLHEVSRLVLDPLQDACRG 480
421 SVSRKSLIFDLLOKQOEARLTLAGLGTQARREPPAPASLHEVSRLVLDPLQDACRG 480
421 SVSRKSLIFDLLOKQOEARLTLAGLGTQARREPPAPASLHEVSRLVLDPLQDACRG 480
481 FYODGRGDRRAKRAKPAKPTGOKMLDLNOKSENPRDLFLMAVILONREHMAITYPMAM 540
481 FYODGRGDRRAKRAKPAKPTGOKMLDLNOKSENPRDLFLMAVILONREHMAITYPMAM 540
481 FYODGRGDRRAKRAKPAKPTGOKMLDLNOKSENPRDLFLMAVILONREHMAITYPMAM 540
541 GQEGVAAALAAACKILKEMSHLETAENARATREAKYERLAL----DLFSECVNSEARA 595
541 GQEGVAAALAAACKILKEMSHLETAENARATREAKYERLAL----DLFSECVNSEARA 595
541 GQEGVAAALAAACKILKEMSHLETAENARATREAKYERLAL----DLFSECVNSEARA 595
541 GQEGVAAALAAACKILKEMSHLETAENARATREAKYERLAL----DLFSECVNSEARA 595
596 FALLVRRNRKWSKTTCHLATEADAKAFPAHDGYQAFITRIMWGDMAAGTILMLLGAFL 655
596 FALLVRRNRKWSKTTCHLATEADAKAFPAHDGYQAFITRIMWGDMAAGTILMLLGAFL 655
596 FALLVRRNRKWSKTTCHLATEADAKAFPAHDGYQAFITRIMWGDMAAGTILMLLGAFL 655
601 FALLVRRNRKWSKTTCHLATEADAKAFPAHDGYQAFITRIMWGDMAAGTILMLLGAFL 659
601 FALLVRRNRKWSKTTCHLATEADAKAFPAHDGYQAFITRIMWGDMAAGTILMLLGAFL 659
656 CFALVYTNLITFSEAPLRTGLDLODLSLDTKSPILYQOSVVEELVEAPRAQGRGP 715
656 CFALVYTNLITFSEAPLRTGLDLODLSLDTKSPILYQOSVVEELVEAPRAQGRGP 715
660 CPALVYTNLITFSEAPLRTGLDLODLSLDTKSPILYQOSVVEELVEAPRAQGRGP 719
716 RAVELLTRMRKFWGAPVTVFIGNVVMYFAFLFTYVLLVDFRPPQSGSGPEVTLYFWV 775

720 RAVELLTRMRKFWGAPVTVFIGNVVMYFAFLFTYVLLVDFRPPQSGSGPEVTLYFWV 779
776 FTVLVEIRGQFFDEDTTHVKKFTLVGDNMKNCDVVALFLFVGTGCMPLBAFEGR 835
780 FTVLVEIRGQFFDEDTTHVKKFTLVGDNMKNCDVVALFLFVGTGCMPLBAFEGR 839
836 TVLAMDPMVFTLRILHIFAIHKOGLPKIIVERMMKDVFFFLPSVWLVAVGTTQALL 895
840 TVLAMDPMVFTLRILHIFAIHKOGLPKIIVERMMKDVFFFLPSVWLVAVGTTQALL 899
896 HPHDGRLEWIFRRVLYRPVYQIFQOIPLDEIDEARVNCSTHPLLEDSPSCSLYANWL 955
900 HPHDGRLEWIFRRVLYRPVYQIFQOIPLDEIDEARVNCSTHPLLEDSPSCSLYANWL 959
956 ILLVTEFLVNTVNLMLLAMSPTVOVQVNA TMWVKORVLYIEYHERPLAPPEI 1015
960 ILLVTEFLVNTVNLMLLAMSPTVOVQVNA TMWVKORVLYIEYHERPLAPPEI 1019
1016 LLSHLSTLBRVFEKEA-----EHRKHLERLPPDLQKVTWTWQENFLSK 1065
1020 LLSHLSTLBRVFEKEAHEHREHGEHREHREHRLPDLQKVTWTWQENFLSK 1079
1066 MEKRRDSEGEVLKRTAHRVDFAKYIGLREDEKRIKLESQINYSVTVSSVADYLAQ 1125
1080 MEKRRDSEGEVLKRTAHRVDFAKYIGLREDEKRIKLESQINYSVTVSSVADYLAQ 1139
1126 GGGPRSSQHGSGSQLVAADHGGIDGMEQPGAGQPSDT 1165
1140 GGGPRSSQHGSGSQLVAADHGGIDGMEQPGAGQPSDT 1179

RESULT 5

AAB86164 standard; Protein: 1158 AA.

AAB86164;

09-AUG-2001 (first entry)

Mouse MTR1 protein.

MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor; transient receptor potential family; BMS; Beckwith-Wiedemann syndrome; 11p15.5 abnormality; chromosome 11; anticancer; developmental activity; intracellular calcium ion regulation; hormone; growth factor; apoptosis; cell growth; cell death; cell differentiation; urogenital disease; polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor; rhabdomyosarcoma.

Mus sp.

W0200132693-A2.

10-MAY-2001.

06-NOV-2000; 2000MO-DE03876.

04-NOV-1999; 99DE-1053167.

(UVGU-) UNIV GUTENBERG JOHANNES.

Prawitt D, Pelletier J, Zabel B;

WPI; 2001-316417/33.

N-PSDB; AAH20623.

DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann

syndrome and tumors, also related proteins and antibodies -

Disclosure; Fig 11; 46pp; German.

This invention describes a novel DNA sequence (I) encoding the MTR1

protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BMS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MRI is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urgent diseases, including polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MRI gene or activity of its protein, or with calcium influx into cells, e.g. BMS, Wilms tumor, rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (II) can also be used for recombinant production of MRI proteins (II) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or anti-DNA antibodies. (II) are used to raise Ab, as reagents in competitive assays for (II), as tissue markers; for identifying interacting proteins and in screening for (anti)agonists. This sequence represents the murine MRI gene described in the method of the invention.

Sequence 1158 AA;

Query Match 83.2%; Score 5068.5; DB 22; Length 1158;

Query Local Similarity 83.9%; Pred. No. 0; Mismatches 109; Indels 13; Gaps 4;

Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

1 MODVGPSPGADRELRRLHGEVFGSGKKRGKRVVPSGAPSVLFDLLAEW 60
1 MOTTSSCGSPPTDDEGMEPLRCGEINFGSGKKRGKRVVPSGAPSVLFDLLAEW 60
61 HLPAPLVVSLVEEOPFPMKSWLDVLRKGLYKAAQSTGAMITLSALVGLARHVGQV 120
61 HLPAPLVVSLVEEOPFPMKSWLDVLRKGLYKAAQSTGAMITLSALVGLARHVGQV 120
61 HLPAPLVVSLVEEOPFPMKSWLDVLRKGLYKAAQSTGAMITLSALVGLARHVGQV 120
121 RHSLASTSTKRVVAVGMAASLGRVLRHRLLE--EAQEPFPHYPPEDGSGGSLCLSDS 178
121 RHSLASTSTKRVVAVGMAASLGRVLRHRLLE--EAQEPFPHYPPEDGSGGSLCLSDS 178
121 RHSLASTSTKRVVAVGMAASLGRVLRHRLLE--EAQEPFPHYPPEDGSGGSLCLSDS 178
179 NLSHFLVPEPPGPKG-DGLTELRLRLERKHSERAGVGGTSGIEIPVLCVLVNGDPNTL 237
181 NLSHFLVPEPPGPKG-DGLTELRLRLERKHSERAGVGGTSGIEIPVLCVLVNGDPNTL 240
238 ERISRAVEQAAPVLLVSGGTAADVLAALVNPPLLVPKAKQFKEKPKSKHFSMEDIV 297
241 ERISRAVEQAAPVLLVSGGTAADVLAALVNPPLLVPKAKQFKEKPKSKHFSMEDIV 300
298 RMTKLQNTSHOHLITVDFEPEGSEELDTVLKALVACKSHSQEPDYLDELALAVA 357
301 HMTLQNTAAHPHLITVDFEPEGSEELDTVLKALVACKSHSQEPDYLDELALAVA 360
358 WDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKEPFRVLPVNDGADVADFLTYGRLOE 417
361 WDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKEPFRVLPVNDGADVADFLTYGRLOE 420
418 LTRSVSRKSLFLFLORKEEARLTLAAGTQOAREPPAPFASLHEVSRVLKDTLQDA 477
421 LVHSVSPKSLFLFLORKEEARLTLAAGTQOAREPPAPFASLHEVSRVLKDTLQDA 480
478 CGGFYODGRGDRRAEKGPAPKPTGOKMLDLNOKSENWRPLFLMAVLQNHMAATF 537
481 CGGFYODGRGDRRAEKGPAPKPTGOKMLDLNOKSENWRPLFLMAVLQNHMAATF 536
538 WAMGQGVAAALACKILKEMSHLETAEARARATREAKYERLALDFSECSYNSSEARAPA 597
537 WAMGQGVAAALACKILKEMSHLETAEARARATREAKYERLALDFSECSYNSSEARAPA 596
598 LTVRRNRCKSKTTLHLATEADAKAPAHQVAFLTRIWMGMAAGTPIRLILGAFPLC 657
597 LTVRRNRCKSKTTLHLATEADAKAPAHQVAFLTRIWMGMAAGTPIRLILGAFPLC 656

658 ALVNTNLTPEEAPLRTGLDLDLDTESKSPYLQSGRVBELVEAPRAGDRGPA 717
657 ALITNLTSPEDAPQRNDLDEPDSLDMEKSFRCGSGQLKLTAPAPAGDLGPA 716
718 VPLLTRMKKEMGAPVTFVGNVVFAPFLFTYVLLVDFPPRPGSGGPEVTLFWVFT 777
717 AFLTRMKKEMGAPVTFVGNVVFAPFLFTYVLLVDFPPRPGSGGPEVTLFWVFT 776
778 LVLEIRGPFPTDDETHLYKKFTLVYGNMKNKCDVAFLEIVGTGCMPLSPAFAGRTV 837
777 LVLEIRGPFPTDDETHLYKKFTLVYGNMKNKCDVAFLEIVGTGCMPLSPAFAGRTV 836
838 LAMPFVNTLRLIHFAHKGKPIIVERMKNKDVFFELFSLVWLVAYVTTQALLHP 897
837 LAIDFVNTLRLIHFAHKGKPIIVERMKNKDVFFELFSLVWLVAYVTTQALLHP 896
898 HDGRLEWTFRRVLYPIQITGQIPLDEIDARVNCSTHPLLEBSPCPSLYANWLVTL 957
897 HDGRLEWTFRRVLYPIQITGQIPLDEIDARVNCSTHPLLEBSPCPSLYANWLVTL 956
958 LTVFLVNTVNLMLLTFMPSYTFQVQGNATMFKFORNYLIVEYHERPALAPPITL 1017
957 LTVFLVNTVNLMLLTFMPSYTFQVQGNATMFKFORNYLIVEYHERPALAPPITL 1016
1018 SHLSLTLRRVPEKKAHREHLERDLPDLDQVVTWETVQKENFLSKMKRRRDSGEV 1077
1017 SHLSLTLRRVPEKKAHREHLERDLPDLDQVVTWETVQKENFLSKMKRRRDSGEV 1076
1078 LRTKARVDFLAKYIGLRBEQKRIKCLSEQINTSVLSVADVLAAQGGRRSSQHCE 1137
1077 LRTKARVDFLAKYIGLRBEQKRIKCLSEQINTSVLSVADVLAAQGGRRSSQHCE 1136
1138 GSQVAAADHRGIDGMEQAGAGPPSDT 1165
1137 RSQPASARD-----EYLSGLPPSDT 1158

RESULT 6
ABB83854
ID ABB83854 standard. Protein; 1158 AA.
XX
AC ABB83854;
XX
DT 30-SEP-2002 (first entry)
XX
DE Mouse ltrpc5 SEQ ID NO 5.
XX
KW Mouse; ltrpc5; taste; cell signalling; TC-ICS; food; pharmaceutical;
KW taste cell-specific ion channel subunit.
XX
OS Mus sp.
XX
PN WO200254069-A1.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US49808.
XX
PR 29-DEC-2000; 2000US-259379P.
PR 21-DEC-2001; 2001US-0026188.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zuker CS, Zhang Y;
XX
DR WPI; 2002-583632/62.
DR N-PSDB; ABB85734.
XX
PT Identifying modulators of taste signaling in taste cells for use in
PT food and pharmaceutical industries to customize and regulate taste, by
PT determining effect of the compound on a taste cell-specific ion channel
PT subunit

PS Claim 1, Page 211; 306pp; English.

XX The invention relates to identifying (M1) a compound that modulates taste
CC signalling in taste cells, by contacting the compound with a eukaryotic
CC host cell or cell membrane which expresses a taste cell-specific ion
CC channel subunit (TIC-1CS), and determining a functional effect of the
CC compound upon a transmembrane ion flux of a predetermined ion.
CC Identifying a compound that modulates taste signalling in taste cells.
CC (M1) is useful for identifying a compound that modulates taste signalling
CC in taste cells, for identifying a compound that binds to a taste cell
CC specific ion channel subunit and for modulating taste signalling in taste
CC cells of a mammal, in particular a human. Modulators identified by (M1)
CC are used by the food and pharmaceutical industries to customize taste,
CC e.g. as additives to food or medicine so that the food or medicine tastes
CC different to the subject who ingests it. Bitter medicines can be made to
CC taste less bitter and sweet substance can be enhanced. The modulators are
CC useful for pharmacological and genetic modulation of taste signalling
CC pathways. The taste modulators can be directly administered to mammalian
CC subjects for modulation of taste in vivo. The present sequence is that of
CC the predicted mouse Itipcs protein of the invention.

XX Sequence 1158 AA;

Query Match 83.2%; Score 5068.5; DB 23; Length 1158;

Beet Local Similarity 83.9%; Pred. No. 0;

Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

QY 1 MODVGGPPSPGPDREDELHGEVNFSGSGKKRKFVVPSPGVA PSVLPDILLMEW 60
DB 1 MOTTOSCPGSPBPDDEDGMEPLKGEINFGSGKKRKFVVPSPVLPFELLTLEW 60
QY 61 HLPAPNLVSLVGEBOFPAMKSWLRLVRLKGLVKAOSTGAMILLTSALRVGLARRVQAV 120
DB 61 HLPAPNLVSLVGEBOFPAMKSWLRLVRLKGLVKAOSTGAMILLTSALRVGLARRVQAV 120
QY 121 RDHSLASTSTKRVYAVAGMAGSLGRVLRRIIE--EAQDFPVHYVEDDGGSGGPRCSIDS 178
DB 121 RDHSLASTSTKRVYAVAGMAGSLGRVLRRIIE--EAQDFPVHYVEDDGGSGGPRCSIDS 178
QY 121 RDHSLASTSTKRVYAVAGMAGSLGRVLRRIIE--EAQDFPVHYVEDDGGSGGPRCSIDS 178
DB 121 RDHSLASTSTKRVYAVAGMAGSLGRVLRRIIE--EAQDFPVHYVEDDGGSGGPRCSIDS 178
QY 179 NLSHFILVEPPGPKG-DGLTELRLRLKHSI SEORAGVGGTSGIIEPIVLCILVNDPMTL 237
DB 181 NLSHFILVESGALSGNDGLTELQSLKHSISQQTGGTGGTSCIDIPVLCILVNDPMTL 240
QY 238 ERISRAVEQAA PWLLILVSGGIADVALVNPQHLVPEKVAEKQEKFPSPKHFSEMDIV 297
DB 241 ERISRAVEQAA PWLLILVSGGIADVALVNPQHLVPEKVAEKQEKFPSPKHFSEMDIV 297
QY 298 RWTKLQNTSHQHLTYDFEQSGSEBLDTVIILKALVYKACKSHSQEPQDYLDKLAFA 357
DB 301 HMTLQNTSHQHLTYDFEQSGSEBLDTVIILKALVYKACKSHSQEPQDYLDKLAFA 360
QY 358 WDRVDIAKSEIFNGGVKSCDLEVMVDALVSNKPEEVRLLFVNDGAVVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIFNGGVKSCDLEVMVDALVSNKPEEVRLLFVNDGAVVADFLTYGRLOE 420
QY 418 LYSRVSRSKSLFDLQKQSEARLTLAGTQQAEPAPGPAFSLHEVSRYLXDFLODA 477
DB 421 LYSRVSRSKSLFDLQKQSEARLTLAGTQQAEPAPGPAFSLHEVSRYLXDFLODA 480
QY 478 CRGTYQDGRPDGRRRAEKPAPKPTGQKWLDDNOKSENPMRDLFLMAVLQNRHEMATYF 537
DB 481 CRGTYQDGRPDGRRRAEKPAPKPTGQKWLDDNOKSENPMRDLFLMAVLQNRHEMATYF 536
QY 538 WAMGOEGVAALAAKCKILKEMSHLETEAARATREAYEELADLFSECSNSGARFA 597
DB 537 WAMGOEGVAALAAKCKILKEMSHLEKEAEVARTWEAEYELADLFSECSNSGARFA 596
QY 598 LLYRRNRCKSKTTCILHLEAEDAKAFPAHDGVOAFLTRIMGMMAAGPPIRLIGAFICF 657
DB 597 LLYRRNRCKSKTTCILHLEAEDAKAFPAHDGVOAFLTRIMGMMAAGPPIRLIGAFICF 656
QY 658 ALVYTNLTISEEAPLRIGLEDLQDLSLDTKESPLYLQSRVEELVAPPAQDGRGPA 717
DB 658 ALVYTNLTISEEAPLRIGLEDLQDLSLDTKESPLYLQSRVEELVAPPAQDGRGPA 717

DB 657 ALIYTNLTISEEDAPQRMLEDLQEPDSLDMKESFLCSRGQLKEXLTAEPAPGDLGPOA 716
QY 718 VFLTRMRKFWGAPVTVFLGVNVMWFAFLPFTVYLVDVPPPPGSPGSEVTLVFWVFT 777
DB 717 AFLTRMRKFWGAPVTVFLGVNVMWFAFLPFTVYLVDVPPPPGSPGSEVTLVFWVFT 776
QY 778 LYLSEIRGFTDEDTLHYKKFTLYVGDNMKNKCMVAIFLPIVGTCTMLPSAFBAGRTV 837
DB 777 LYLSEIRGFTDEDTLHYKKFTLYVEDNMKNKCMVAIFLPIVGTCTMVPVSFEAGRTV 836
QY 838 LAMPVWTLALHIFAIHAKOLGKXIIVERNKMDVFFFLPSVWLVAVYTTQALLHP 897
DB 837 LAIFEMFTLRIHIFAIHAKOLGKXIIVERNMKDVFFFLPSVWLVAVYTTQALLHP 896
QY 898 HDGRLEMTFRVLRVPYQIRGOIPLDEIDARVNCSTHPLLEDSPCSPSLYANWLYL 957
DB 897 HDGRLEMTFRVLRVPYQIRGOIPLDEIDARVNCSTHPLLEDSASCPULYANWLYL 956
QY 958 LVTFLVTVNLNMLNLIAMFSYTFQVQVGNATVFWKFORYNLIVEYHERPALAPFTLL 1017
DB 957 LVTFLVTVNLNMLNLIAMFSYTFQVQVGNADVFWKFORHLYVEYHGRPALAPFTLL 1016
QY 1018 SHLSILTRVVKKAHEKREHLERDLPPLDQKVTMETVOKENFLSMERRRDSEGEV 1077
DB 1017 SHLSILVTKOVRKEAOKRQHLERDLPPLDQKVTMETVOKENFLSMERRRDSEGEV 1076
QY 1078 LRKTAHRYDPIAKYLGRLBQEKRIKLESQINVCVSVSVAVLACGGPSSQHCCE 1137
DB 1077 LRKTAHRYDPIAKYLGRLBQEKRIKLESQANVCMLLSMTDTLAPGGTYSSQNCGC 1136
QY 1138 GSQLVAAADHRGIDGWEOPGAGOPPST 1165
DB 1137 RSQPASARDR-----EYLSGLPSPDT 1158

RESULT 7
AAB86166 ID AAB86166 standard; Protein; 1158 AA.
XX AC AAB86166;
XX DT 09-AUG-2001 (first entry)
XX DE Mouse MTR1 protein #2.
XX MT1, TRP-related protein; β 2+ regulation; calcium regulation; tumor;
XX transient receptor potential family; BMS; Beckwith-Wiedemann syndrome;
XX 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
XX intracellular calcium ion regulation; hormone; growth factor; apoptosis;
XX cell growth; cell death; cell differentiation; urogenital disease;
XX polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
XX rhabdomyosarcoma.
XX Mus sp.
XX OS
XX WO200132693-A2.
XX PN 10-MAY-2001.
XX PD
XX 06-NOV-2000; 2000WO-DE03876.
XX PF
XX 04-NOV-1999; 99DE-1053167.
XX PR
XX (UYGU-) UNIV GUTENBERG JOHANNES.
XX PA Prawitt D, Pelletier J, Zabel B;
XX PI WPI; 2001-316417/33.
XX DR
XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies -
XX PS Disclosure; Fig 12; 46pp; German.

598 LLVRNRCSKTTCLHLATEADAKAFFAHGVOAFLTRIWGDMAGTPILRLGAF LCF 657

DR WPI; 2002-017608/02.

RESULT 8	
AAMS1707	
ID	AAMS1707 standard; Protein; 1157 AA.
XX	
AC	AAMS1707; .
XX	
DT	16-JAN-2002 (first entry)
XX	
DE	Mouse TRP8.
XX	
KW	Mouse; human; TRP8; transient receptor potential channel;
KW	taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
KW	pharmaceutical.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 467
FT	/note= "Encoded by CACGAG"
XX	
PN	WO200179448-A2.
XX	
PD	25-OCT-2001.
XX	
PF	17-APR-2001; 2001WO-US12608.
XX	
PR	17-APR-2000; 2000US-197491P.
PR	13-APR-2001; 2001US-0834792.
XX	
PA	(MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX	
PI	Margolskee RF, Huang L, Rong M, Max M, Perez CA;
XX	
DR	WPI; 2002-017608/02.

DR N-PSDB: AA199707.
 XX A new transient receptor potential channel, designated TRP8, is
 PT expressed in taste receptor cells and associated with perception of
 PT bitter and sweet taste, and is useful to find new flavour enhancers
 XX
 PS Claim 8; Fig 2; 55pp; English.
 XX The invention relates to a mouse and human transient receptor potential
 CC channel, TRP8, expressed in taste receptor cells and associated with the
 CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
 CC flavour enhancers in foods, beverages and pharmaceuticals.
 XX
 SO Sequence 1157 AA;
 Query Match 83.0%; Score 5053; DB 23; Length 1157;
 Best Local Similarity 83.8%; Pred. No. 0;
 Matches 979; Conservative 66; Mismatches 109; Indels 14; Gaps 5;
 QY 1 MODVQPPPGSPGDAEDRRELGLHGEVNFSGSGKRGKRVFVPSGVAHSVLFLLLEW 60
 DB 1 MOTTOSCPGSPPTDEDEMEPILCRGEINFGSGKRGKRVFVPSVAFELLLEW 60
 QY 61 HLPANLVSVLGEERPFAMKSWLMDVLRKGLVKAAOSTGAMILTSALRVGLARVQAV 120
 DB 61 HLPANLVSVLGEERPFAMKSWLMDVLRKGLVKAAOSTGAMILTSALRVGLARVQAV 120
 QY 121 RDHSLASTSTKRVVAVGMAISGRVLRHRIE--BAQDFPVHYPEDDGSQGPLCSLDS 178
 DB 121 RDHSLASTSTKRVVAVGMAISGRVLRHRIE--BAQDFPVHYPEDDGSQGPLCSLDS 180
 QY 121 RDHSLASTSTKRVVAVGMAISGRVLRHRIE--BAQDFPVHYPEDDGSQGPLCSLDS 180
 DB 121 RDHSLASTSTKRVVAVGMAISGRVLRHRIE--BAQDFPVHYPEDDGSQGPLCSLDS 180
 QY 179 NLSHFILVEPBPBGK-DGTELRLRLKHSISQRTGYGTSICQIPVLCILVNDPNTL 237
 DB 181 NLSHFILVEPBPBGK-DGTELRLRLKHSISQRTGYGTSICQIPVLCILVNDPNTL 240
 QY 238 ERISRAVQOAPWILVSGGGLADVLALVNPQPHLLVKNVAKQKKEKFPKSHSEMDIV 297
 DB 241 ERISRAVQOAPWILVSGGGLADVLALVNPQPHLLVKNVAKQKKEKFPKSHSEMDIV 300
 QY 298 RWTKLQVITSHOHLTYVDFEFGSEELDTYILKALVKACSHSQEPQDYLDLKLVA 357
 DB 301 HTTELQVITSHOHLTYVDFEFGSEELDTYILKALVKACSHSQEPQDYLDLKLVA 360
 QY 358 WDRVDIAKSEIFNGDVEKSCDLEEVNDALVSNKPEFVRLFVDNADVADFLTYGRLOE 417
 DB 361 WDRVDIAKSEIFNGDVEKSCDLEEVNDALVSNKPEFVRLFVDNADVADFLTYGRLOE 420
 QY 418 LYRSVSRKSLPDLQKQEBARLTLAGLGTQOAREPPAGPPAFSLHEVSRYLQFLQDA 477
 DB 421 LYHSVSPKSLFELLQKQEBARLTLAGLGTQOAREPPAGPPAFSLHEVSRYLQFLQDA 479
 QY 478 CRGFQODRPGDRRAEKPAKPTGOKMLDLNOKSNPMRDLPLMVLQNRHMAIYF 537
 DB 480 CRGFQODRPGDRRAEKPAKPTGOKMLDLNOKSNPMRDLPLMVLQNRHMAIYF 535
 QY 538 WAMGEGVAAALAAACKILKEMSHLETTEAARATREAKYERLADLFSECYNSSEARAF 597
 DB 536 WAMGEGVAAALAAACKILKEMSHLETTEAARATREAKYERLADLFSECYNSSEARAF 595
 QY 598 LLYRNRKWSKTTCTHATLATEADAKAFPAHDGQVAFTRIWMGMAAGTPILRLGAPLCF 657
 DB 596 LLYRNRKWSKTTCTHATLATEADAKAFPAHDGQVAFTRIWMGMAAGTPILRLGAPLCF 655
 QY 658 ALVYTNLTFSBEAPLRTGLDELQDLSDLTEKSLYLGQSRVEVLVAPRAQGRGPR 717
 DB 656 ALVYTNLTFSBEAPLRTGLDELQDLSDLTEKSLYLGQSRVEVLVAPRAQGRGPR 715
 QY 718 VFLLTRMRKFGAPVTFVGNVVFATFLFTVYLVDFPFPPOGSPGSEVTLVFWFT 777
 DB 716 AFLFLTRMRKFGAPVTFVGNVVFATFLFTVYLVDFPFPPOGSPGSEVTLVFWFT 775
 QY 778 LVLEIRGQFTTDEDTLVKKFTLVYGNWAKCMVAIFLPIVGYTCMVLPSAFAGTIV 837

DB 776 LVLEIRGQFTTDEDTLVKKFTLVYEDNKNKCMVAIFLPIVGYTCMVLPSAFAGTIV 835
 QY 838 LAMDFMVFTLRIHIFAIHKQLGPKIIVERMMKDVFFFLFSYMLVAVGTTQALLHP 897
 DB 836 LAIDFMVFTLRIHIFAIHKQLGPKIIVERMMKDVFFFLFSYMLVAVGTTQALLHP 895
 QY 898 HDGRLEWIFRRVLYRPIYQIQGQIPLDEIDARVNCSTHPLLEDSPSCSLYANWLVYL 957
 DB 896 HDGRLEWIFRRVLYRPIYQIQGQIPLDEIDARVNCSTHPLLEDSPSCSLYANWLVYL 955
 QY 958 LLYVFLVTNVLNMLNLIAMSYFOVVOGNAATMFKRQVNLVYEHYRALAPFTLL 1017
 DB 956 LLYVFLVTNVLNMLNLIAMSYFOVVOGNAATMFKRQVNLVYEHYRALAPFTLL 1015
 QY 1018 SHLSLTLRVPKAEHREHLEERDLPDLPQKVTWETVOKENFLSKERRRDSGEV 1077
 DB 1016 SHLSLTLRVPKAEHREHLEERDLPDLPQKVTWETVOKENFLSKERRRDSGEV 1075
 QY 1078 LRKTAHRVDLTAKYIGLREQEKRIKCLSQINYSVLVSSVADVLAAQGGPRSSQHC 1137
 DB 1076 LRKTAHRVDLTAKYIGLREQEKRIKCLSQINYSVLVSSVADVLAAQGGPRSSQHC 1135
 QY 1138 GSQVAAADHRCIDGWEQPGAGOPPSDT 1165
 DB 1136 RSQPASADR-----EYLSGLPPSDT 1157
 RESULT 9
 ABB83853
 ID ABB83853 standard; Protein, 1164 AA.
 XX ABB83853;
 AC ABB83853;
 DT 30-SEP-2002 (first entry)
 XX
 DE Rat L-TRP SEQ ID NO 2.
 XX
 KM Rat; L-TRP; taste; cell signalling; TC-ICS; food; pharmaceutical;
 KM taste cell-specific ion channel subunit.
 OS Rattus sp.
 XX
 PN MO200254069-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001MO-US49808.
 XX
 PR 29-DEC-2000; 2000US-259379P.
 PR 21-DEC-2001; 2001US-0026188.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Zuker CS, Zhang Y;
 XX
 DR WPI; 2002-583632/62.
 DR N-PSDB; ABN85732.
 XX
 PT Identifying modulators of taste signalling in taste cells for use in
 PT food and pharmaceutical industries to customize and regulate taste, by
 PT determining effect of the compound on a taste cell-specific ion channel
 PT subunit
 XX
 PS Claim 1; Page 63; 306pp; English.
 XX
 CC The invention relates to identifying (M1) a compound that modulates taste
 CC signalling in taste cells, by contacting the compound with a eukaryotic
 CC host cell or cell membrane which expresses a taste cell-specific ion
 CC channel subunit (TC-ICS), and determining a functional effect of the
 CC compound upon a transmembrane ion flux of a predetermined ion,
 CC identifying a compound that modulates taste signalling in taste cells,
 CC (M1) is useful for identifying a compound that modulates taste signalling
 CC in taste cells, for identifying a compound that binds to a taste cell

specific ion channel subunit and for modulating taste signaling in taste cells of a mammal. In particular a human. Modulators identified by (M1) are used by the food and pharmaceutical industries to customize taste, e.g. as additives to food or medicine so that the food or medicine tastes different to the subject who ingests it. Bitter medicines can be made to taste less bitter and sweet substance can be enhanced. The modulators are useful for pharmacological and genetic modulation of taste signaling pathways. The taste modulators can be directly administered to mammalian subjects for modulation of taste in vivo. The present sequence is that of the rat L-TRP protein of the invention.

CC Sequence 1164 AA;

Query Match 81.9%; Score 4988.5; DB 23; Length 1164;

Best Local Similarity 82.6%; Pred. No. 0; Mismatches 116; Indels 11; Gaps 3;

Matches 963; Conservative 76; Mismatches 116; Indels 11; Gaps 3;

1 MODVGPSPGSGDADREELGHRGEVNFSGSGKKRKFVRVPSGVAPVFLDILAEW 60
 9 MEMAASSCGSPPTDGDGHEPVLCGEVNFSGSGKKRKFVRVPSGVAPVFLDILAEW 68
 61 HLPAPNLVSLVGESEOPFAMKSWLRDLVRKGLVKAQSTGANILTSALRVGLARHVQAV 120
 69 HLPAPNLVSLVGESEOPFAMKSWLRDLVRKGLVKAQSTGANILTSALRVGLARHVQAV 128
 121 RHSLASTSTKRVYAVGMAISGRVLRHRIIEAODEPVRVYBEDDGSQGLSDSL 180
 129 RHSLASTSTKRVYAVGMAISGRVLRHRIIEAODEPVRVYBEDDGSQGLSDSL 188
 181 SHFIVEPSPGSGDADREELGHRGEVNFSGSGKKRKFVRVPSGVAPVFLDILAEW 239
 189 SHFIVEPSPGSGDADREELGHRGEVNFSGSGKKRKFVRVPSGVAPVFLDILAEW 248
 240 ISRAVEQAAPWILVSGGSIADVLAALVNPVLPVKAQEKQKPEKPSKHSWEDIVK 299
 249 MSRAVEQAAPWILVSGGSIADVLAALVNPVLPVKAQEKQKPEKPSKHSWEDIVK 308
 300 TLLNITSHOHLTVYDFEORGESELDVILKALVKAQKSHSOEPDYLDELKLAIVAM 359
 309 TLLNITSHOHLTVYDFEORGESELDVILKALVKAQKSHSOEPDYLDELKLAIVAM 368
 360 RVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLVFNDAVDVDFLYTGRLOELY 419
 369 RVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLVFNDAVDVDFLYTGRLOELY 428
 420 RSVSRKSLFDLLQKQKQEARLTLAGLGTQQAEPAPGPAFSLHVSRYLKDPLDADR 479
 429 HSVSPKSLFELLERKHEGRLLTAGLGAQOTRKLFGVGLPAFSLHVSRYLKDPLDADR 488
 480 GFYQDGRPDRRRAEKGAPKPTGQKWLIDNOKSENPMRDFLMVLGNRHEMATYFMA 539
 489 GFYQDGRPDRRRAEKGAPKPTGQKWLIDNOKSENPMRDFLMVLGNRHEMATYFMA 544
 540 MGOEVAALAAACKILKEMSHLETEAARATREAKERYLALDLPSECYSNSEARAFALL 599
 545 MREGVAALAAACKILKEMSHLEKEAFAVARTREAKERYLALDLPSECYSNSEARAFALL 604
 600 VRRNRCSYTTCLHATEADAKAFPAHGVQAFVLRIMWGDMAAGTPIIRLLGAFICPAL 659
 605 VRRNRCSYTTCLHATEADAKAFPAHGVQAFVLRIMWGDMAAGTPIIRLLGAFICPAL 664
 660 VTNLTITSEBEAPLRTGLDLDLSDLPDEKSPLYGLQSRVLELVNAPAQDGRGRAPV 719
 665 IYTNLTITSEBEAPLRTGLDLDLSDLPDEKSPLYGLQSRVLELVNAPAQDGRGRAPV 724
 720 LTRMRKFGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLFVFWFTLV 779
 725 LTRMRKFGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLFVFWFTLV 784
 780 LEEIRGFTFDETHLVKFTLVVGNWKNCDMAVIFLFTVGTGCMLEPSAFAGRTVLA 839
 785 LEEIRGFTFDETHLVKFTLVVGNWKNCDMAVIFLFTVGTGCMLEPSAFAGRTVLA 844

840 MDMFVETRLIHIFAIHKQLGPKIIVVERMMKDVFFFLFPLSVMLVAVGVTTOALLPHD 899
 845 IDFMVETRLIHIFAIHKQLGPKIIVVERMMKDVFFFLFPLSVMLVAVGVTTOALLPHD 904
 900 GRLEWIFRRVLYRPLQIFGQIPLDEIDEARVNSTHLLLEDSPSCSLYANMVLITLL 959
 905 GRLEWIFRRVLYRPLQIFGQIPLDEIDEARVNSTHLLLEDSPSCSLYANMVLITLL 964
 960 VTFLLVTVLMLNLIAMFSTFOVVOGNATMFMKFORYNILVEXHERPALAPPITLISH 1019
 965 VTFLLVTVLMLNLIAMFSTFOVVOGNATMFMKFORYNILVEXHERPALAPPITLISH 1024
 1020 LSLTRRVFKKEAEKREHLEBRDLPDLOKRVWTVETVOKENFLSKEMKRRDSEGVLR 1079
 1025 LSLTRRVFKKEAEKREHLEBRDLPDLOKRVWTVETVOKENFLSKEMKRRDSEGVLR 1084
 1080 KTAHRVDIATYKIGLREGEKRIKLEQINVCISLVSVADVLAQGGSPSSQCGSGS 1139
 1085 KTAHRVDIATYKIGLREGEKRIKLEQINVCISLVSVADVLAQGGSPSSQCGSGS 1144
 1140 QLVADHRGGIDGMEQPGAGPPSPT 1165
 1145 QPASADR-----EYLAGLPHSDT 1164

RESULT 10

AAB86163 standard; Protein; 872 AA.

AAB86163;

09-AUG-2001 (first entry)

Human MTR1 protein without exon 18 fragment.

MTR1, TRP-related protein; Ca²⁺ regulation; calcium regulation; tumor; transient receptor potential family; BWS; Beckwith-Wiedemann syndrome; 11p15.5 abnormality; chromosome 11; anticancer; developmental activity; intracellular calcium ion regulation; hormone; growth factor; apoptosis; cell growth; cell death; cell differentiation; urogenital disease; kidney polycystic kidney disease; calcium influx; Wilms tumor; thalidomide tumor; thalidomide sarcoma.

Homo sapiens.

WO200132693-A2.

10-MAY-2001.

06-NOV-2000; 2000MO-DE03876.

04-NOV-1999; 99DE-1053167.

(UYGU-) UNIV GUTENBERG JOHANNES.

Prawitt D, Pelletier J, Zabel B;

WPI; 2001-216417/33.

N-PSDB; AAH20574.

DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies -

Claim 10; Fig 4; 46pp; German.

This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis

Query Match 39.9%; Score 2430.5; DB 23; Length 1166;
 Best Local Similarity 45.4%; Pred. No. 2.1e-221;
 Matches 532; Conservative 177; Mismatches 352; Indels 111; Gaps 26;

26 GEVNGSGGKRGKRVVPVSPVLPDILLAEVHLPAFNLVSLVGECPFANKSMIR 85
 28 GELDTGACRKSNLRSLDRTPDAVYSLVTRTGAFAPNLVSLVGGSGPVLTQMLQ 87
 86 DVLARKGLVKAOSTGAMILTSALRVGLARHVGQAQVADHSLASTSTKRVVAVGMSLGRV 145
 88 DLLRRGLVAAOSTGAMIVTGLHTGIGHVGVAAVRDHQMASTG-GTKVAVAGVAPWGVV 146

146 LHRRLLEKQEDFPVHY-----PEDDGGSGPLCLSDLSLHFIIVPEBPCKGDLTEL 200
 147 RRRDRLINPKGSPARYRMRGDEP--GVQFP--LDVYSAFVLDDGTGCLGGENRF 201

201 RLRLKHLSEOPAGYGTGSIPIVLCILVNGDPMTLERISRAVEQAFMLIVSGGIA 260
 202 RLRLSEYISQKTVGCTG-IDIPVLLILDDGDKMLTLENATQALPCLLVAGSGGA 260

261 DVLALVNPGLLP-----KVAKQPKPKPSKHSFWMEDIVRWTKLLQNTSHOLL 313
 261 DCLAEFLD--TLAPSGGARGQEARDRIRFFPK-----GDLVLAQVERIMTRKELL 313

314 TVYDPEQESSELDVYILKALVKACKSHQEPQDYLDELKLVAMDRVDAKSEIFENGDV 373
 314 TVYSSD-DSSEETVTLALVAC--GSSEASAYIDELRLVAMNRVDAIOSELRGDI 370

374 EWKSCDLEEVMDALVSNKPEFVRLFDVNGADVADELTVYRLOELVRSYRSKSLFDLQ 433
 371 QMRSPHLEASLMDALINDRPEFRLILSHGLSHGLTLMRLAQLYSAPNSLIRNLLD 430

434 RKOEARLTLAQL--GTQAREBPAGRPAPSLHEVSRVTKDFLOACRGFYODGRPDNR 491
 431 QASHSAGTAPALKGAALRP-----DVGHVLRMLGKVCARYSGGAMDH 480

492 RAEKGAKPRTGKMLLDNOKS-----ENPRDLFIWAVLONRHEMATYFAMQ 542
 481 ----PGQFGESWYLLSDKATSPSLDLGAGLPDILLVLMRLQMANVTFEMWS 535

543 EGVAAALACKILKEMSHLETEEAARATREA--KYERLALDLSECYNSSEARAFALV 600
 536 NAVSSALGACILLRVWARLEPDEBARAKDLAFKEGCVLDLFGCYSSSEVBARALL 595

601 RNRNCSKTTCHLATEADAKAFPAHDGVQAFITRIWGMMACTPILRLGALFCFALV 660
 596 RRCPLMGDATCIQLAMQADARAFADGVOSLITOKMWMGMSTPIWALVLAFCPLI 655

661 YTNLTF--SEAPLRTGLDLODLSLDTESPLVGLQSRVELVEAPAOQD----- 712
 656 YTRLITFRKSEEPTEBELE--FDMDSVINGECPGTADPAEKTPIGVPRQSRPCCGG 713

713 --RGPRAVELLITRMRFKAGAPVTVLGNVVPAPFLFTVYLLVDFRPPQSPGSEVY 770
 714 RCGRRG---LRMHFWGAPVITIFMGNVSVYLLFILFISRVLVDFQAP--PGLLELL 768

771 LYFWVTVLVEIRQGFTEDETF-----HLVKFTLVGDNMKCMVAFLPI 819
 769 LYFWATTLCEELRQGISGGGSLASGPGPHASLSQRILVLAIDSMOCDLVALTCFL 828

820 VGTTCMLSPAFAGRPVLAAMDVFTLRILHFAHKLQGPRTIIVERMKVDFPLF 879
 829 LGVGCRLTPGLYHGRVLCIDIMVFTVRLHITVKNQGPRTIVKMKVDFPLF 888

880 LSVMLVAVGVTQALLPHDGRLEWIFRRLVYRPIYQIFQDILDEIDARV--NCSTH 936
 889 LGMVLVAVGATGLRPRSDPSILRRFYRPIYDIFQIDQEDMDVLAHMSNCSSE 948

937 PLLLEDS-----SCBSLVANMLVILLVTFLLVTVNLLNLLIAMSSTFYQVQGNAM 991
 949 PGFWAHPGQAQAGTCVAGVANNMLVLLLVIFLLVANILLVLLIAMSSTFYQVQGNL 1008

992 FMKFORVNLIVEHERPALAPPFILLSHLTLRRVFK-----EAHKREHLERD 1042
 1009 YMKQGRVLIIEFHSRPLAPPFIVISHLRLLQLCRPPSPQSSPALHFRVYLSKE 1068

1043 LPDPLDKVTVTWETVQENFLSKMEKRRRDSGEVLKRTAHVPFIKYLGLAEQEKRI 1102
 1069 ----AERKLTWESVHNENFLARARDREDSRLKTSQVDLALQOLCHIREYQRL 1124

1103 KCLSEQINVCVLSVADVLAQG-----GGP 1129
 1125 KVLEREVOQCSRVLGVAEALSRGALLPPEGP 1156

RESULT 12
 ID AA95436
 AA95436 standard; Protein; 1214 AA.

AA95436;
 10-OCT-2000 (first entry)

Human calcium channel SOC-3/CRAC-2.
 SOC-3/CRAC-2; calcium channel; human; store operated channel;
 calcium release activated channel; therapy; diagnosis;
 lymphocyte proliferative disorder.

Homo sapiens.
 WO20040614-A2.
 13-JUL-2000.

20-DEC-1999; 99WO-US29996.
 30-DEC-1998; 98US-0114220.
 29-JAN-1999; 99US-0120018.
 22-JUN-1999; 99US-0140415.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 Scharenberg AM;
 WPI; 2000-465957/40.
 N-PSDB; AAA49923.

New SOC/CRAC calcium channel polynucleotides and polypeptides used to
 diagnose and treat proliferative disorders associated with the channel,
 and to screen for novel modulators of the channel

Claim 14; Page 100-103; 108pp; English.

The present sequence is that of human SOC-3/CRAC-2, a member of
 a novel family of store operated channel (SOC) or calcium release
 activated channel (CRAC) polypeptides that modulate Ca2+ flux into
 and out of a cell, and which may be activated upon depletion of
 Ca2+ from intracellular calcium stores, allowing Ca2+ influx into
 a cell. SOC-3/CRAC-2 is expressed predominantly in colon and kidney.
 Compositions for expressing functional SOC/CRAC calcium channel
 polypeptides in cells are expected to be useful for treating
 patients that have reduced extracellular calcium influx into their
 SOC/CRAC-expressing cells. They will also be useful for delivering
 therapeutic and/or imaging agents to such cells to modulate
 proliferation and growth. SOC/CRAC polypeptides also represent
 targets for designing and/or identifying inhibitors that block
 lymphocyte proliferation and binding agents that selectively bind
 to SOC/CRAC polypeptides to which drugs or toxins can be conjugated
 for delivery to SOC/CRAC expressing cells. Methods for determining
 the level of SOC/CRAC expression in a subject can be used to assess
 the presence, or absence, or stage of a proliferative disorder,
 e.g. a lymphocyte proliferative disorder.

Sequence 1214 AA;


```

QY 86 DYLKRGVKAASGTAMILTSALRGVLAHNGQAVRDSHASTSTKRVAVAGMASLGRV 145
DB 136 DLRRLGVAAPAASTAMVLTGTLTGIGHVAVARHQMASTG-GTKVAVAGVAPWGV 194
QY 146 LHRRLIEEAQEDFPVHY-----PEDDGSQGLCSLDSNLSHFILVEPGRPGKGLTEL 200
DB 195 RNRDLINPKGSFPARYRWRGDEPD--GVQFP--LDVYSAFPLVDQTHCCLGENNF 249
QY 201 RLRLKHSIEQAGYGGTSGSIEIPVLCILVNGDPNTERISPAVEQAQWMLLVSSGGA 260
DB 250 RLRLSISYISQKTVGGTSG-IDIPVLLLLIDDEKMLTRIEVATQAOQLPCLLVASGGGA 308
QY 261 DVLALVNGPHLLVP-----KVAEKQKPKSHFPMEDIVMTKLLQNTSHOHL 313
DB 309 DCLALTELD--TLAPSSGARGQEARDRIRREPK-----GDLEVLQAOVERIMTKELL 361
QY 314 TVYDEEQESELDTVILKALVACKSHSQEPQDYLDELKLAAMDVDAKSEIFNGDV 373
DB 362 TVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYIDELRLAVAMNRVDIAQSELFRDI 418
QY 374 EKKSCDLEEVWDALVSNKPEFVRLFDNGADVADFLTYGRIQELYSVSRSKLLFDLIQ 433
DB 419 QMRSPHLEASLMDALINDRPEFVRLISHGLSHFLPMRLAQYSAAPSNSLIRNLID 478
QY 434 RKOEARLTLAQL--CTQOAREPPAPPAFSLHESVRVLDLQDAGCFYODGRGDR 491
DB 479 QASHSAGTKAPALKGAAELRPP-----DVGHVLRMLGKMKCAPRYSGGAMDH 528
QY 492 RAEKGPAPKPTGQKMLLDLNOKS-----ENPRDLFLVAVLONRHEMATYFWAMQ 542
DB 529 -----PGCGFESMYLSDKATSPSLDAGLGQAPSDLLMALLLNRAQWMPYEMGS 583
QY 543 EGVAAALAAKILKENSHLETEEAARATREA--KYERLALDFSCYCNSEARAPALLY 600
DB 584 NAVSSALGACLLIRVWARLEPDAAARRKDLAFKEGEGVDLFGCYSSSEARARLL 643
QY 601 RNRCKSKTTCCHLAEADAKAFAHDGVQAFLTRIMWGDMAQFTLLIGLFCFALV 660
DB 644 RRCPLMGATCLOLAQADARAFPAODGVOSLTQKMWGDMASTTIALVLAFFCPPLI 703
QY 661 YTNLTF--SEAPLRTGLDLDLSDLTEKSPLYGLOSVELEAPRAQD----- 712
DB 704 YTRLIFRKSSEEPREBLE--FDMOSVINGESPVTAPAEKTPGLGVROSGRPCGG 761
QY 713 --RGRAVFLTRKRFWGAIVTVFLGNVVMFAFLFTTYVLLVDFRPPQSGCEVY 770
DB 762 RCGGRRC--LRWFHFGVPTVIFMGNVSYLLFLLFSRVLLVDFOPAF--PGLLEL 816
QY 771 LTFWTVLLEETROGFTEDETF-----HLVKKFTLYVGNMNMCDWVAIFLEFI 819
DB 817 LTFWATLCEELRQGLSGGGSLASGCPGPHASLSQRRLVLAQSMOCDVATCTH 876
QY 820 VGVTCMLPSAFAGRTVLAMDPMVTLRLIHFAIKOLGPKIIVERMMKDVFFELF 879
DB 877 LGVGLTLTGVLHGTVCIDIMVTVRLHLHFTYNKOLGPKIVSKMKOVFFELF 936
QY 880 LSVMLVAVGVTQALLPHDGRLEWIFRRVLYRPIYQIQGLPLDEIDARV--NCSTH 936
DB 937 LGVMLVAVGVALEGRLRPRSDPSPILRFRPYRPIQIQOIQOEDMDVALMHSCSS 996
QY 937 PLLLESP-----SCPSLVANMVLVILLVTVLTVNVLNMLLIANFSYFOVQGNATM 991
DB 997 PGFWAHPGAQACTCVSOYANMLVLLVFLVAVNLNMLLIAMFSYFGVQGNASD 1056
QY 992 FMKFORVNLIVEXHRRPALAPPFILSHSLTRRVFK-----EAHHRKHLERD 1042
DB 1057 YMAQYRLIRHSHRPALAPPITVSHLLRLQLCRRRSPQSPSPALHHRVYLSL 1116
QY 1043 LPDPLDQVVTWTVQKENFLSKMEKRRDSESEVLAKTARVDIATAKVTGILREDEKRI 1102
DB 1117 ----AERKLLTWESVHKENFLARARDKRESDESRILKRTSQKDLAKQIGHIREYORL 1172

```

```

QY 1103 KCLSEQINVCVSVSVADWLAQ-----GSP 1129
DB 1173 KVLREYVQCGSRVLGWAVALSRSLALPPGSP 1204

```

```

RESULT 14
ID AAB85974
ID AAB85974 standard; Protein; 1129 AA.
XX
AC AAB85974;
XX
DT 30-NOV-2001 (first entry)
XX
DE Human TLCC polypeptide.
XX
KW TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
KW hepatotropic; cardiac; antiarteriosclerotic; antiinflammatory; vitruide;
KW cytosolic; analgesic; cerebroprotective; nootropic; neuroprotective;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1084..1129
FT /note="the residues in this region are not indicated in
FT the sequence present in the sequence listing, but
FT indicated in the Figure"
XX
PN WO200162794-A2.
XX
PD 30-AUG-2001.
XX
PE 20-FEB-2001; 2001WO-US05529.
XX
PR 22-FEB-2000; 2000US-0510706.
PR 31-MAY-2000; 2000US-0583373.
PR 08-AUG-2000; 2000US-0634669.
XX
PA (MILL-) MILENNIUM PHARM INC.
XX
PI Glucksmann MA, Curtis RAJ, Lora JM;
XX
DR WPI; 2001-557700/62.
XX
DR N-PSDB; AAH76383, AAH76384.
XX
PT New isolated nucleic acid encoding a transient receptor potential-like
PT calcium channel for identifying modulators that can be used to treat
PT hepatic or cardiovascular disorders.
XX
PS Claim 14; Fig 1A-D; 160pp; English.
XX
CC The invention provides isolated nucleic acids encoding a human transient
CC receptor potential (TRP) family member, called TRP-like calcium channel
CC (TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC recombinant methodology. The TLCC polynucleotides and polypeptide are
CC used to identify modulators that can be used to treat a hepatic or a
CC cardiovascular disorder, such as liver fibrosis or atherosclerosis.
CC Other disorders that can be treated are hepatitis, liver tumors,
CC cirrhosis of the liver, hemochromatosis, liver parasite induced
CC disorders, central nervous system disorders, pain disorders, or
CC disorders of cellular growth, differentiation or migration. The TLCC
CC polynucleotides, polypeptide, protein homologs and antibodies to the
CC protein can be used in predictive medicine (e.g. diagnostic assays),
CC prognostic assays; monitoring clinical trials and pharmacogenetics).
CC Anti-TLCC antibodies can isolate TLCC proteins, regulate the
CC bioavailability of TLCC proteins, and modulate TLCC activity. The
CC present sequence represents the human TLCC polypeptide.
XX
SO Sequence 1129 AA;

```

```

Query Match 39.3%; Score 2394.5; DB 22; Length 1129;
Best Local Similarity 45.4%; Pred. No. 5-5e-218;
Matches 526; Conservative 174; Mismatches 348; Indels 111; Gaps 26;

```

```

OY 39 KFRVPSGVAHSVLFDDLLAEHNLDPNLVSVLGEEOFPAMKSNLRLVLRKGLVKAQS 98
D 4 QFLRLSDRTDPAVAVSLVTRTWGFPANLVVSVLGGSGAPVLQTVLQDLRLRGLVRAQS 63
OY 99 TGAUMLTALAVGLARHVGQAVRDSLASTSTKRVAVVAGMASLGRVLRRLLEAODEF 158
D 64 TGAUMLTALAVGLARHVGQAVRDSLASTSTKRVAVVAGMASLGRVLRRLLEAODEF 122
OY 159 PVHY-----PEDDGSOGPLCSLDNSLHFLIVERGPGKGGLTELRLLEKHSIORA 213
D 123 PARIRMRDPEB--GVQFP--LDVNSAFPLVDGTGTCGCGEKRFRRLRESYSIOQKT 177
OY 214 GYGGTGSIIEPVLCLVNGDPNTERISRAVEQAAPMLIVGSGGIADVLAALVNOPIHL 273
D 178 GVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAQPCILLVAGSGAACLATLEDD--TL 234
OY 274 VP-----KVAEKPFKEKPSKHSWEDIYRWTLQNTSHOULLVYVPEQSGSEL 326
D 235 APGSGGARQGEARDRIRRFPPK-----GDLEVLQAQVIRIMTRKELLTVYSGE--DGSSEF 288
OY 327 DTVLKALVKAACKSHOPEODVDELKLAVAMDRVDAKSEIFNGDVKMSDLEEWMD 386
D 289 ETIVUKALVKAAC--GSSASAYLDDELRLAVAMNRVDLQSEIFRGDITQKSFHLIASLMD 346
OY 387 ALVSNKPEFVRLFVNDGADVADFLTYGRLOELVRSVSKSLFDLLQKQEBARLTLAGL 446
D 347 ALVNDREFVRLLSHGLSLGHFLIPMLAQVYSAAPNSLIJRLNLDQASHSAGTKAPAL 406
OY 447 --GVOQAEPPAGPPAFSLHEYSRLKDFLODAGCGFQDGRPGRRRAEKGPAPKPPGQ 504
D 407 KGGAAELPP-----DVGHVLRMLGMCAPRPPSGGAMPB-----PGGPFES 451
OY 505 KMLDLNOKS-----ENPWRLFLMAVLQNHENMATYFWAMGQGVAAALAAKIL 555
D 452 MYLLSDKATSPSLDAGLGQAHPMSDLLMALNLNPAQAMTFWENGSAVSSALCACL 511
OY 556 KEMSHLETEAARATREA--KYERIALDLFSECSYNSSEARAFALLVNRNCSKTTCLH 613
D 512 RVMARLEPDAEBAARXKDLAFKFBGMVDLFGECRSEVAARLLRLRCPIMGDATCLQ 571
OY 614 LATEADAKAFPAHGVQAFTRIMWGMAAGTPILRLGAPLCFALVYTNLITP--SEEA 671
D 572 LAMQADAFAPFAODGVOSLITQKWWGMASTPIALVALAFCCPLIYTRLITPFKSEB 631
OY 672 PLRGLLEBLODLSLDEKSPLYGLQSVVEELVEBPAQD-----RGRANFLITR 723
D 632 PTRBELB--FMDSVINGEPVGTADPAEKTPLVGPVROSGRPGCCGRCGARCC--LRR 686
OY 724 WRKFWGAPVTVFLGNVVMYFAFLFLFTYVLLVDPPRPGQSGPSEVTVYFWVFTLVLEI 783
D 687 WPHFWGAVTIFMGVNVSVLFLFLFSRLVLDPPRPA--FQSELELLIYFAFTLICEEL 744
OY 784 ROGFETDEBT-----HLVKFTLVYGDNNKNCMDVAIFLIVGTCRMLPSAFE 832
D 745 ROGLSGGGGSLASGPGPGHSLSQRLRYLADSWNQCIDLVALTCFLGVCGRILPGLYH 804
OY 833 AGRTVLAMDPMVFTLRILHIFAIHOKLGPKIIVERBMKDVFFELFELSVMLVANGVTQ 892
D 805 LGRTVLCIDPMVFTVRLHIFVNLKQDGPKITVYSKMKDVFFELFELGVMVLAAGVATE 864
OY 893 ALLPHRDLEMIFFRVLVYRPLQIFQOIPLDEIDEARV---NCSTHPLLEDSF----- 944
D 865 GLLRPRDSDFSLRLRVYRPLQIFQOIPOEDMVALMEHNSGSEGFMAHPGGAAG 924
OY 945 SCPSLYANMVLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLV 1004
D 925 TCVSQYANMVLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLVTLV 984
OY 1005 HERPLAPPFILSLTLRVRPK-----EAHKKSEHLERDLPDLQGVVYWE 1055
D 985 HSRPALAPPFVISHLRLKQCRPRSPPOSSPALHEFRVYLSKE---AERKLTWE 1040

```

```

OY 1056 TVQKENFLSKMEKRRDSEGEVLKRTAHRVDLFIKVLGGLREOSKRIKLESQINYSGL 1115
D 1041 SYHKEFNFLAARBRKEDSRLKRTSQVDLALQGHIREYORLKVLEREVQCCSRV 1100
OY 1116 VSSVADVLAAQ-----GGP 1129
D 1101 LGWVAEALSRALLPPGP 1119

RESULT 15
ABG72088
ID ABG72088 standard; Protein, 1083 AA.
XX
XX ABG72088;
AC
XX 11-FEB-2003 (first entry)
DT
XX
DE Human transient receptor potential (TRP)-like calcium channel (TLCC).
XX
XX Human; transient receptor potential-like calcium channel; TRP;
XX TLCC; 18607; calcium signalling; growth; differentiation;
XX capacitative calcium channel; store-operated calcium channel; SOC;
XX plasma membrane; calcium ion; cytosol; modulator; membrane excitability;
XX action potential; excitation; neurite outgrowth; synaptogenesis;
XX signal transduction; angiogenesis; cell proliferation; vascular tone;
XX gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;
XX rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;
XX central nervous system disorder; Alzheimer's disease;
XX Parkinson's disease; multiple sclerosis; epilepsy; cancer;
XX cellular proliferation disorder; migration disorder; therapeutic.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Region 1..1083
FT /note= "This region is shown as SEQ ID NO:2 in the
FT sequence listing of the specification, but is only
FT a shorter version of SEQ ID NO:2 shown in figure.
FT 1"
XX
XX US2002142377-A1.
XX
XX 03-OCT-2002.
XX
XX 20-FEB-2001; 2001US-0789481.
XX
XX 22-FEB-2000; 2000US-0510706.
XX 31-MAY-2000; 2000US-0583373.
XX 08-AUG-2000; 2000US-0634669.
XX
XX (GUDC/) GLUCKSMANN M A.
XX (CURT/) CURTIS R A J.
XX (LORA/) LORA J M.
XX
XX Glucksmann MA, Curtis RAJ, Lora JM;
XX
XX WPI; 2003-102516/09.
XX N-PSDB; ABS58041.
XX
XX Isolated transient receptor potential-like calcium channel
XX polypeptide, useful for treating cardiovascular, hepatic, central
XX nervous system disorders, pain, cellular proliferation, or migration
XX disorder.
XX
XX Claim 14; Fig 1; 80pp; English.
XX
XX The invention discloses an isolated transient receptor potential
XX (TRP)-like calcium channel (TLCC) polypeptide (18607). Calcium signalling
XX has been implicated in the regulation of a variety of cellular responses,
XX such as growth and differentiation. TLCC is a member of the capacitative
XX calcium channel group or store-operated calcium channel (SOC) which is
XX activated in the plasma membrane to import calcium ions from the

```

extracellular environment to the cytosol. The nucleic acids, polypeptides and antibodies of TLCC are useful for detecting its presence in a sample, for identifying a compound which binds to it and identifying a compound which modulates its activity. Modulators of TLCC can be used to modulate membrane excitability, wave forms and frequencies of action potentials, thresholds of excitation, neurite outgrowth and synaptogenesis, signal transduction, angiogenesis, endothelial cell proliferation and vascular tone. The nucleic acid and polypeptide are also useful (using gene therapy) for diagnosing and treating cardiovascular disorders, such as atherosclerosis and restenosis, endothelial cell disorders, such as tumor metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic disorders such as hepatitis and cirrhosis, central nervous system disorders, such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and epilepsy, cellular proliferation disorders, such as cancer, and growth, differentiation or migration disorders. TLCC can also be used in predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics) and in methods of treatment (e.g. therapeutic and prophylactic). The sequence presented is the human TLCC, 18607, protein.

Sequence 1083 AA;

Query Match 38.3%; Score 2335; DB 24; Length 1083;
Best Local Similarity 45.7%; Pred. No. 2.4e-212;

Matches 513; Conservative 165; Mismatches 338; Indels 106; Gaps 25;

```

QY 39 KRVVSSGAVPVLFFLLAEWHLPRNVLVSLVGEQFPAMKSWLDVLRGIVYAAQS 98
DB 4 QPLRLSDRTDPAVSVLVRTRWGFRAPLVSVLGGSGPVLQTLWQDILLRGLVVAAS 63
QY 99 TGAMITSLARVGLARVGAOAVRDHSLASTSTKRVVAVAGMASLGLVLRRIIEAQEDF 158
DB 64 TGAMITVGLHRTGIGHVAVRDHOMASTG-CTKVAAGVAPWGVRRRDTLIPKXSF 122
QY 159 PVHY-----PEDGSGQGPLCSLDSNLSPHILVEPQPGKDGTLRLRLKHHISQRA 213
DB 123 PARYWRGDPED--GVQFP---LDVYNSAFPLVDDGTHGCLGGENFRRLLESYSIQKT 177
QY 214 GVGCGSTIPIVLCILVNDGPNLTLEISRAVEQAAPWILVNGSGIADVLAALVNPPLL 273
DB 178 GVGCGT-IDIPVLLIDDEKMLTRLENATQAOLPCLLVAGSGADCLAEITLED--TL 234
QY 274 VP-----KVAEKQPEKPEPSKGFMSWDIVRTWTKLLQNTSHOHLITVYDEQSGSEL 326
DB 235 AAGSGGARGEARDRIRREFPK-----GDEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288
QY 327 DTVILKALYACKSHSQEPQDYLDELKLAVMADRVDAKSEIFNGDEVKSCDLEEVMD 386
DB 289 ETIVLKALYAC--GSSEASAYLDELRLAVAMNRVDIAQSELPFGDIOWRSFHLIASLMD 346
QY 387 ALVSNKPEFVRFLVNDGAVADFLTYGRLOELYRSVRKSLPFDLLQKQEARLTLAQL 446
DB 347 ALLNDPEFVRLLISHGLSLGHFLTPWRLAQLVSAAPSNSLIRNLLDQASHSAGTYAPAL 406
QY 447 --GTQARPPAPPAFSLHEVSRVLKDFLODACRGFYODGRPGDRRAEKGPAPRTQ 504
DB 407 KGAALRPP-----DVGHVLRMLGKMCAPRYPGGAWDPH-----PGQFGES 451
QY 505 KMLLDLNQKS-----ENPWRDLFLVAVLQNRHEMATYFWAMGOEGVAAALAACTIL 555
DB 452 MYLLSDKATSPSLDAGLGOAPWSDLLWMLLNRAOMAMYFWMGSNNAVSSALGACLL 511
QY 556 KEMSHLETAEARARAREA--KTERLALDLPSECYSNSEARAPALLVRRRCWSTKTC 613
DB 512 RVVARLEPPAEARAKDLAFKFEQGVDFGECYRSSEVRARALLLRCPIMGDATCLO 571
QY 614 LATEADAKAFPAHDGVAFLTRIMGDMAGTPIRLGAFLCFALVYTNLITF--SEEA 671
DB 572 LAMQADARAFRQDQVQSLLTQKMGDMASTIYALVLAFCPPILYTRILITFRKSEEB 631
QY 672 PLRTGLEDLDDSLDTEKSPLYGLQSRVELVEAPRAQD-----RGPRAVFLTR 723
DB 632 PTREBLE--FDMDSVINGEPVGTADPAEKTPGVVPRQSGRPCCGRCGRC---LRR 686

```

```

QY 724 WRKFWGAVTVLGNVVMYFAFLFETVLLVDRPPQGSQSGEVTLTFVWFTLVLEBI 783
DB 687 WFFWGAVTTFMGNVSYLFLFLFSRLVLDVQPA--FGSLELLIYFNAFTLLCEBL 744
QY 784 RQGFTEBDT-----HLVKKFTLYYGDNNKCDMAVLFETIVGTCRMLPASAE 832
DB 745 RQGLSGGGGSLASGPGGHASLSQRLLRYLADSNOCDLVALTCFLLGVCGRTPGGLYH 804
QY 833 AGRTLANDFWFTLRLLHFAIKHKGAPKTIYVERMKDVFPLFPLSVMLVAYGVTQ 892
DB 805 LGRTVLCIDFWFVTRLLHFTVKNQDLPKTVISKMKMDVFFLFLGVLVAAGVATE 864
QY 893 ALLHPDRLEWIFPRVLYRPLYQIFQOIPLDEIDARV---NCSTHPLLEDSP----- 944
DB 865 GILRRDDPFSILRVRVRYRPLQIFQIPOEDMVALMEHSNCSSEBGFMAHPRGAQAG 924
QY 945 SCPSLYANMVLILLVTLVTVNVLMLLAMPSTYFQVVOGNAWTFMKFORVNLIVEY 1004
DB 925 TCVSQYANWLVLLLVIFLVANILLVNLIAMFSYTFGKVOGNDLYWKAQRYRLREF 984
QY 1005 HERPALAPPTLLSLTLRVPFK-----EAEKHKEHLERDLDPDLDOKVVTME 1055
DB 985 HSRPALAPPTLVISHRLRLQLCRPRSPQSSPALHFRVYLSKE---AEKRLTWE 1040
QY 1056 TVOKENPLSKMKRRRDSGEVLRKTAHVDPIAKYLGLRE 1097
DB 1041 SVHKENFLARARDKRESDSERLKTTSOKVDLALKQDHIHE 1082

```

Search completed: September 10, 2003, 09:39:43
Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 10, 2003, 09:38:44 ; Search time 21 Seconds
(without alignments)
2347.245 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6051
Sequence: 1 MQDVQGRPRGPGDAEDRRE.....HRGGIDGWEOPGAGQPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/aa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/aa/Backfilltest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041	33.5	1503	US-09-600-087-2	Sequence 2, Appli
2	1562.5	25.7	1095	US-09-112-096-15	Sequence 15, Appli
3	1228.5	20.2	1533	US-08-623-679-9	Sequence 9, Appli
4	1228.5	20.2	1533	US-08-933-774-9	Sequence 9, Appli
5	1228.5	20.2	1533	US-09-181-030-9	Sequence 9, Appli
6	1228.5	20.2	1533	US-09-534-242-9	Sequence 9, Appli
7	1228.5	20.2	1533	US-09-454-854-9	Sequence 9, Appli
8	1228.5	20.2	1533	US-09-164-671-9	Sequence 9, Appli
9	1150.5	18.9	1497	US-08-623-679-7	Sequence 7, Appli
10	1150.5	18.9	1497	US-08-933-774-7	Sequence 7, Appli
11	1150.5	18.9	1497	US-09-181-030-7	Sequence 7, Appli
12	1150.5	18.9	1497	US-09-534-242-7	Sequence 7, Appli
13	1150.5	18.9	1497	US-09-454-854-7	Sequence 7, Appli
14	1150.5	18.9	1497	US-09-164-671-7	Sequence 7, Appli
15	813	13.3	315	US-09-020-956-112	Sequence 112, App
16	813	13.3	315	US-09-030-607-112	Sequence 112, App
17	813	13.3	315	US-09-439-313-112	Sequence 112, App
18	813	13.3	315	US-09-352-616A-112	Sequence 112, App
19	813	13.3	315	US-09-232-148A-112	Sequence 112, App
20	606	9.9	300	US-08-727-688-11	Sequence 11, App
21	504.5	8.3	316	US-09-412-431-3	Sequence 378, App
22	498	8.2	542	US-08-412-431-3	Sequence 3, Appli
23	498	8.2	542	US-08-623-679-3	Sequence 3, Appli
24	498	8.2	542	US-08-933-774-3	Sequence 3, Appli
25	498	8.2	542	US-09-181-030-3	Sequence 3, Appli
26	498	8.2	542	US-09-534-242-3	Sequence 3, Appli
27	498	8.2	542	US-09-454-854-3	Sequence 3, Appli

28	498	8.2	542	4	US-09-164-671-3	Sequence 3, Appli
29	333.5	5.5	201	4	US-09-461-325-175	Sequence 175, App
30	285	4.7	256	2	US-08-727-688-33	Sequence 33, Appli
31	221	3.6	742	4	US-09-500-123-12	Sequence 12, Appli
32	216	3.5	871	4	US-09-500-123-7	Sequence 7, Appli
33	210.5	3.5	1709	4	US-09-392-812A-6	Sequence 6, Appli
34	201.5	3.3	1619	4	US-09-392-812A-4	Sequence 4, Appli
35	186	3.1	1704	4	US-09-392-812A-2	Sequence 2, Appli
36	180	3.0	811	4	US-09-500-123-9	Sequence 9, Appli
37	171	2.8	116	4	US-09-461-325-375	Sequence 375, App
38	153	2.5	761	3	US-09-235-451-4	Sequence 4, Appli
39	150	2.5	968	3	US-08-651-999A-7	Sequence 7, Appli
40	150	2.5	968	3	US-09-385-752-7	Sequence 7, Appli
41	143.5	2.4	843	4	US-09-235-451-25	Sequence 25, Appli
42	142	2.3	839	4	US-09-667-422-4	Sequence 4, Appli
43	141	2.3	839	3	US-09-197-636-2	Sequence 2, Appli
44	141	2.3	839	3	US-09-197-636-8	Sequence 8, Appli
45	141	2.3	839	4	US-09-235-451-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-09-600-087-2
; Sequence 2, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6548272yoshi
; APPLICANT: Nagamine, Kenharo
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
; FILE REFERENCE: 11283-004001
; CURRENT APPLICATION NUMBER: US/09/600,087
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: PCT/JP99/06289
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JP/321200/1998
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (320)...(344)
; NAME/KEY: TRANSMEM
; LOCATION: (750)...(773)
; NAME/KEY: TRANSMEM
; LOCATION: (794)...(818)
; NAME/KEY: TRANSMEM
; LOCATION: (867)...(891)
; NAME/KEY: TRANSMEM
; LOCATION: (900)...(924)
; NAME/KEY: TRANSMEM
; LOCATION: (932)...(956)
; NAME/KEY: TRANSMEM
; LOCATION: (1024)...(1048)
US-09-600-087-2

Query Match 33.5%; Score 2041; DB 4; Length 1503;
Best Local Similarity 36.8%; Pred. No. 2,1e-191;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGSGKKRGRFVRVPSGVAPSVLFDLLAEWHLPAPIVLVSLVGEQPFAMKSWLR 85
DB 128 GDIVFTGSLGQVKKVVRVSGDTPSSVIVHLMTQMGDLPVLLISVTGAKVFMKKPRLL 187
QY 86 DVLRKGLVKAQSGATWLTSLAKVGLARHVGQAVRHSLSASTKRVAVAGMAGSLGRV 145
DB 188 SIFRGLVKAQSGATWLTSLAKVGLARHVGQAVRHSLSASTKRVAVAGMAGSLGRV 247

146 LHRRLLEAEQEDPVHYEPEDGSGOGLCSLDSNLSHFLVPERGPGKDGTELRLE 205
 248 HREBGLIHFTGSPFAEYIIDEBOG--QGNLTCGLDSNLSHFLVDGTHGQGVGVEIPLRTRE 306
 206 KHISEORAGYGTGSIETPCLLVNGDPNTERISRAVEQAAPWILVGGGADVLAA 265
 307 KEISEOTKERGV-AIKIPICVVLGEGGTLHTIDNATNGTPCVAVGSGRADVLAQ 365
 266 LVNQP--HLLVPAVKEQ--FKERPSGHFEMEDIVRTKLLONTSHOHLTVYDFQ 320
 366 VNNLPVSDTITSLIQKLSVFFOEMET--FTESRIVETTKKIQDVRRLTLVREBK 423
 321 ESSEEDTVILKALVAKCSHSEOPDYLD-EIKLAVANDRYIAKSEIFNGDVEWKS 379
 424 DQGVADVAILQALAKSROHFGHEMNDHOKLAVANNRDIARSELFMEMQKRPD 483
 380 LEEVAVDALVSNKPEFVRLFVNDGADVADPLTYGRLOELYSVSRKSLFDLLQKREBA 439
 484 LHPMTAALISNKPFEVRLFLENGVQLKEFTWDTLLYENLDPSCLFHSKLOK----- 538
 440 RLTLAGLGTQOAREPPAGP--PAFSLHEVSRVLKDLQACGFGYODGRPGDRR----- 492
 539 -----LVLEDPERPAAPAPRLOMHHVAQVREHLSGFTPLPRPHNDRLRLLEPV 592
 493 -----AEKPAKPTGQKWLIDLNQKSENPWRLFLVAVLONRHEMATYFWAMQ 542
 593 PHVKLVGVSLSRLYKSSGHVTF-----TMDPRDILLVAVONRRELGLIITWAGQ 646
 543 EGVAAALAAKLIKEMSHLETEAAR--ATREAKYERLALDLFSECSNSEBARAFALL 599
 647 DCIAALACSKILKEISEEDTDSSEEMALAE-EYEHRAIGVFTECRKKEEBAQKLL 705
 600 VARNQWSTTGLHATEADAKAFPAHDGVOAFLRIMWGDMAAGPIRLILGALFCFL 659
 706 TVSEAMGKTTCQLALEKMKFVSHGSIQAFELTKVMGQSLVDNGLRVLCLMAFL 765
 660 VYTNLTTFSEEARPLRTGEDLDLSDLEKSPLYGLQSRVEELVEAPRAQDGRPAVF 719
 766 LITGLISPREKR-----LQD-----VGTFA----- 786
 720 LITRMKFGADVTVFLGNVVMFAFLFTYVLVLDPRPPOGSGPVTLYFVFTLV 779
 787 ---RAAFETAAVVVFNHILSYFAFLCLFAYLAWDFQV--PSMCECAIYLMFSLV 840
 780 LEEISGFEETDTHLYKFFLYVGNMKNKCDMVAELFIVGTCMILSABAGTVLA 839
 841 CEEMKQLFYDPBECGLMKKALYFSDFMKLDVGLILFVAGLTCRLIATLYPGKVLIS 900
 840 MDPVFTLLIHLIHAHKOLOGPKIIVEREMKDVFFFLFSLVWLAVAGVTTQALLPHD 899
 901 LDFILFCRLMHIFITSKLGPKIIIVKMKDVFFFLFLAVVVSFCVAAQALIHNE 960
 900 GLEWIFRRVLYRPYQITGQIP--LDEIDEARVNS--THPLLEDSPCS----- 948
 961 RAVDMLFRAVVHNSYTLIFGOIPGYIDGVNFPEHSPNGTDPY----RPKPSPDATQO 1016
 949 --LVANWLVILLYPFLVTVNLMMLLAFMSYTGVOVGNATMFKORNLIEYHE 1006
 1017 RAAPFWMVLVLLCTLFTNLILLNLILAMENYTFQOVQEHDDQIMKQORHDLLEHNG 1076
 1007 RPAAPFILLSHLSTLLRVPFKEAENKREHLEBDLPDLQKVTVTEVOKENFLSK 1066
 1077 RAAPRPFILLSHLOFIRKVVILKTPAKHKOKNLEKNEBALSWEIYLKENVLOQR 1136
 1067 EKRRDSBGEVLAKTAHADVFLAKVY-----GGLREOKRIKLESQINCVSLVSS 1118
 1137 QCOQORPEOKIEDISNKVDAMVDLIDPLKRSQSM---EORLASLEQVAVQATARALHM 1193
 1119 VADVLAQGGRRSSQHCSEGSQVLAD---HGGIDGWEOPG 1157
 1194 IVRTLASGSSSEADVPTLASQAABEPDAEPGRKRTKEPG 1235

RESULT 2
 US-09-112-096-15
 ; Sequence 15, Application US/09112096
 ; Patent No. 6194152
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiner Laus
 ; APPLICANT: Michael H. Shapiro
 ; APPLICANT: Larisa Tsavalier
 ; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
 ; TITLE OF INVENTION: Antigen Compositions
 ; FILE REFERENCE: 7636-0015.30
 ; CURRENT APPLICATION NUMBER: US/09/112,096
 ; EARLIER FILING DATE: 1998-07-09
 ; EARLIER APPLICATION NUMBER: 60/056,110
 ; EARLIER FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: fastseq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 1095
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-112-096-15
 Query Match 25.7%; Score 1562.5; DB 3; Length 1095;
 Best Local Similarity 34.2%; Pred. No. 2.1e-144;
 Matches 378; Conservative 202; Mismatches 394; Indels 111; Gaps 27;
 26 GEVNFSGSKRGKRVPRVSGVAPVLEFDLLAEWHLPAPMLVVSVEGEOPFAMKWL 85
 95 GDIOGETLGGK-GKTRISCTDDELIVELLOHMLTPMLVSVTGAKAFALKPRK 153
 86 DVLRKGLVKAQSTGAWILTSALRYGLARHYGOAVRDHSLASTSTKYVAVGMAAGLV 145
 154 KIFSR-LVYIQQSKAMWIDGTHGLTKYGEVVRDNTI--SRSEENI VALIGAMGV 211
 146 LHRRLLE--EAQEDPVHYEPEDGSGOGLCSLDSNLSHFLVPERGPGKDGTELR 202
 212 SNRDTLINCAEGFYLAQYLMDD-FTRDPLYIIDNNHTHLLVNDGCHGPTVEAKLRN 270
 203 RLEKHISE--ORAGYGTGSIETPVCLLVNGDPNTERISRAVEQAAPWILVGGSGI 259
 271 QLEKHISRTTODSNYVG---KIPVCFAGCGKETIKAINTSIKKIPCVVSGSRI 326
 260 ADVLALVNOPHILVPAKAEKQFKEKFS--KHFSMEDIVWTKLLONTSHOHLTVYD 317
 327 ADVISLVEVEDAPTSAAVKEKLVPRVTSRSEETSEMIKWLKELILOGSHLLTVIK 386
 318 FEQESSELDTVILKALVAKCSHSEOPDYLDLKLAVANDRYIAKSEIFNGDVEWKS 377
 387 MEAEDEIVSNALISVALYKASTSEQDKDNNGQKLLEWNOQLDANDEIFTNDRWES 446
 378 CDLEEVMDALVSNKPEFVRLFVNDGADVADPLTYGRLOELYSVSRKSLFDLLQ---R 434
 447 ADLQEVMTFALIKDPKFTVRLFLENGLWLRKFLTHDVLTFL-SNHSSTLVYRNLIQAKN 505
 435 KOEBA RLTLAGLGTQOAREPPAGPAPFSLHEVSRVLKDLQACGFGYODGRPG--DRRA 493
 506 SYNDALLTF-----VMTLVANFR---RGFKKEDBNGRDENDI 539
 494 EKPAKPTGQKWLIDLNQKSENPWRLFLVAVLONRHEMATYFWAMQOEGVAAALAAK 553
 540 E-----LHDSVPITRHPLOALFIWAILONKKELSKVIEOTRGCTLALAGASK 587
 554 ILKEMSHLETEAARARREA--KYERALLDLFSCYNSSEARAFALLVRNRRCWKTTC 611
 588 LKTLAKKNDIINAEGSEBELANEYETRAVELFTECYSSDDEDLQOLLVYSCAAGGSNC 647
 612 LHLATEADAKAFPAHDGVOAFLRIMWGDMAAGPIRLILGALFCFALVYTNLTTFSEA 671
 648 LELAVEATDQHTAOPQONFLSKOMYGEISROTGMWIIICLFIPIVGGGFGVFRKK- 706
 672 PLRTGLIEDLDLSDLEKSPLYGLQSRVEELVEAPRAQDGRPAVFLLTRMKFWGAP 731


```

:      MOLECULE TYPE:  protein
us-08-623-679-9

Query Match      20.2%  Score 1228.5;  DB 1;  Length 1533;
Best Local Similarity 27.9%;  Pred. No. 3,66-111;
Matches 356;  Conservative 229;  Mismatches 451;  Indels 241;  Gaps 38;

QY  40  FVRVPSGASVSLFDLLLAEWHLPAPIVLVSLVGESEPPFAMKSWLRDVLARKGLVKAQST  99
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   2  YIRSYDTKPPSLHLVAKDMQLELPKLLISVHGGLGNFENQPKYKQVFGKGLIKAAMTT  61
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY  100 GAWILTSALRVGLARHVGQAVRDHSLASTSTKQVRVAVGNASLGRVLRRLRLEEAOEDF-  158
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   62 GAWLFTGGVSTGCVISHGDALKDH---SSKSRGVCAIGIAPKGV-----ENKEDLV  111
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY  159 ---FVHYPEDDGSGQGPLCSIDSNLSHFPIIVEPQPPGKDGLTCLRRLRLEKHSIQ-  211
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   112 GKQVTRVYQMSNLSKLSVLNNSHTFFILADNTLTQYGAEYVLRRLRLEHGISLQKINT  171
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY  212 PAGVGTGSGIEIPVLCILLVNGDPNTLIERISRAVEQAAPWILV--GSGGIADVLA-----  264
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   172 RLGG-----VPLVGLVVEGGPQVAVSLVLEVLQEEPPIPVLCIDGSGGRASDILSPAHKY  225
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY  265 ---ALVNO--PIILVPAKAEQKQKPPSKPEKSWEDIYRWTKLLONTSHQHLTVYD  317
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db   226 CEEGGINESLREQTLV--TIQTKFNFNKQAQSHQLPAIMECK-----KKELVTVFR  276
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY  318 FEQGSSELDTVILIKALVKACKSHSQEPDYLDLKLAVAMDYDIKASEIFNGDVEW-  375
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

Db      897 LYFVIMLVLMSPGVARQALHPHEE-KPSWKLARNIFPMYMYIGEYFADQID----- 950
Qy      933 CSTDHLLLEDSPSC-----PSLVANMLVILLVTFILVTNVLNMLLIAMFS 979
Db      951 ----LYAMEINPPCGENLYDEGKRLPCTPGAMLTPLMACYLLVANILLVANLIAVFN 1006
Qy      980 YTFQVQGNATPMFQFORNYLIVEYHERPALAPFILLSLTLRV---FKKEAEHNR 1036
Db      1007 NTFEEVKISINQVMKFORQOLMTFHDRLVLPMPILISHIYIIMRLSGCRKCRKREGDQ 1066
Qy      1037 EHLEBDL-----PDLQDKVVTWETVQENFLSKMEKRRRDEGEVLKRTAHVDFIAXY 1091
Db      1067 EERDRGLKFLPSDEELKHLHFEEOCVQEHFREK-EDEOQSSSDERIRVTSERVENMSMR 1125
Qy      1092 LGLREOEK-----RIKLESQINCSVLSSVADV-----LAQGGPSSQHCQ 1136
Db      1126 LEEINERETFMKTSLOTVDLRLAQLBELSNRVNVALENLAGIDRSDLIQARS-RASSSEC- 1183
Qy      1137 EGSQVLADHRGIDGM 1153
Db      1184 EATYLLROSSINSADGY 1200

RESULT 4
US-08-933-774-9
; Sequence 9, Application US/08933774A
; Patent No. 6025137
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; FILE REFERENCE: 07314/004003
; CURRENT APPLICATION NUMBER: US/08/933,774A
; EARLIER FILING DATE: 1997-09-19
; EARLIER APPLICATION NUMBER: US 08/623,679
; EARLIER FILING DATE: 1996-03-29
; EARLIER APPLICATION NUMBER: US 08/412,431
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: PRF
; ORGANISM: Homo sapiens
US-08-933-774-9

Query Match      20.2%; Score 1228.5; DB 3; Length 1533;
Best Local Similarity 27.9%; Pred. No. 3.6e-111;
Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38;

Qy      40 FVRVPSGVAHSVLFULLLAEMHLPANLVSLVGEQPPAMKSWLRDVLKGLVYRAQST 99
Db      2 YRVSVDTRKPDLSLHLMVMDQWOLEPKLLISVHGQJQNFEMQPKQVPGKGLIKRAMTT 61
Qy      100 GAMILTSLRVGLARHVAQVARDHSLASTSTKVAVAVGMASIGRVLHRIIEBAQEDF- 158
Db      62 GAMITFGVSTGVISVIGALKDH---SSKSRGRVATIGIAPMGV-----ENKEDLV 111
Qy      159 ---PVHYPPDDGSGQGPLCSDLSNLSHFLVBERPGPKDGLTELRLLEKHISEO--- 211
Db      112 GKDVTRVYQTMENPLSKLSVLNNSHTFILDNGTLGKYGAEVKLRRLLEKHIISOIKINT 171
Qy      212 RAGVGTGSIETIPVLCILVNGDPNTERISRAVEQAAPMLILV---GSGGIAYLA----- 264
Db      172 RLGGQ-----VPLVGLVVEGGPNVSVILEYLQEEPPPIPVVICOSSGASDILSFAHKY 225
Qy      265 ----ALVNO---PHLLVPKAEKQFKEKPPSKHFMEDIVRWTKLLQNTSHOHLTVYD 317
Db      226 CEEGGIINSLREQLLV--TIQKTPYNNQAQSHOLFALIMECKM-----KKELVTVYR 276
Qy      318 FEOGSEELDTVILKALVACKSHSQEPDYLDELKLAVAMRVDIKSEIFNGDEVW-- 375
Db      277 MSEGGQODIEMALITLLKLG--TNVSAF-----DQSLALAMRVDIARSQIFVFGPHWTP 330

```

```

Qy      376 -----KSCD----- 379
Db      331 LGSILAPPTDSKATEKEKKRPPAATTKGGRGKGGKGGKGVKEVEEBEETPRKIELMLMVNA 390
Qy      380 LEEVVDALVSNKEFEYRLFVQNGADVADFLTYYGLOELYRSVSRKSLFDLLOKQDEA 439
Db      391 LEOAMLDALVLDVADVFKLLIENGVMQHFLLTIRLEELVYNTLRGPPTLHLVADVVK 450
Qy      440 RLTLAGLCTQARERPPAPAF--SIHEVSVLDFLODAR-----GFYQD 484
Db      451 NL-----PDYHISLDIGLVLELWKGAYRCNTRKNFTLYNNLGP 494
Qy      485 GRP-----GDRRAEKGPAKPTGQKMLLDN-----QKSENPWRDLFLMAVLQNR 530
Db      495 KRPKALKILGMEDEDEPPAKGKKKKKKKEEEDIDVDVPAVSPQYPPHELMVAVLWKR 554
Qy      531 HEMATYFWAMQOEGVAALAAKILIKENSHLETEAA-----RATEAKYERLALDLF 584
Db      555 QKMAVFLWQGEESMAKALVACKLYKAMAHESSESDLVDDISQDLNNSKDFGQLATELL 614
Qy      585 SECYNSAARAFALLVRRNRCMSKTCGLHATENDAKAFPAHDGQAFLTRIMWG--DMA 642
Db      615 DQSYKHDEQIAMKLTLYELKWNMSNSTCKLVAAGHRDFIAHTCSQMLLTMMWGRLEMR 674
Qy      643 AGTPIRLIGAFLCFALVYTNLITFSEBAPRTGLEDDLODLSLDTKSPLYGLOSRVEE 702
Db      675 KNPGLKVMIGLILPPTILFLEFRIT-----DPSYOTSKENEDGKEEEN 720
Qy      703 L--VEAPRAQD-----RGPAVFLTRMRKFWCAPVTELVGNVMYFAFLFTTYLL 754
Db      721 TDANADASRRKDEEENHKORSIPGKICEFYNAIPVKEWPFYISYGLLTFNVYIL 780
Qy      755 VDFRPPGSGEPETLVFWVFTLVLEIRGFFDEBETHLYKKRTLVVGNMNCMDVA 814
Db      781 VRM--DCWPSLQEIETIVSYVSLALEKIRE-ILMSEBCKLSQKIKVWLQETWNTITDLVA 836
Qy      815 IFLFIVGTCTMMLBSAFBA-GRTVLAMDPMVFTLRILHIFAIHKQIGPKIIVEREMKDV 873
Db      837 ISTPMIGAILRLQNPYMGGRVYICVDIIFMYIRVLDIFGVNKYLGIVMMIGMMDM 896
Qy      874 FFFLFELSVLVAAGVTTQALLPHDGRLEW-IFRRVLYRPLYQIIFGOIPLDEIDEARVN 932
Db      897 LYFVIMLVLMSPGVARQALHPHEE-KPSWKLARNIFPMYMYIGEYFADQID----- 950
Qy      933 CSTDHLLLEDSPSC-----PSLVANMLVILLVTFILVTNVLNMLLIAMFS 979
Db      951 ----LYAMEINPPCGENLYDEGKRLPCTPGAMLTPLMACYLLVANILLVANLIAVFN 1006
Qy      980 YTFQVQGNATPMFQFORNYLIVEYHERPALAPFILLSLTLRV---FKKEAEHNR 1036
Db      1007 NTFEEVKISINQVMKFORQOLMTFHDRLVLPMPILISHIYIIMRLSGCRKCRKREGDQ 1066
Qy      1037 EHLEBDL-----PDLQDKVVTWETVQENFLSKMEKRRRDEGEVLKRTAHVDFIAXY 1091
Db      1067 EERDRGLKFLPSDEELKHLHFEEOCVQEHFREK-EDEOQSSSDERIRVTSERVENMSMR 1125
Qy      1092 LGLREOEK-----RIKLESQINCSVLSSVADV-----LAQGGPSSQHCQ 1136
Db      1126 LEEINERETFMKTSLOTVDLRLAQLBELSNRVNVALENLAGIDRSDLIQARS-RASSSEC- 1183
Qy      1137 EGSQVLADHRGIDGM 1153
Db      1184 EATYLLROSSINSADGY 1200

RESULT 5
US-09-181-030-9
; Sequence 9, Application US/09181030
; Patent No. 625157
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION

```



```

QY 159 ---PVHPEDDGSGPCLSDSNLSHFILVEPPGKGDGLTELRLEKHSIQ----- 211
DB 112 GKDVTIRVOTMNPSTKLSVLNNSHTHFLADNGLGKGAHVXKRLLEKHSIQKINT 171
QY 212 RAGYGTGSGIEIPVCLLVNGDPNTERISRAVEQAAPWLLIV--GSGGIADVLA----- 264
DB 172 RLGQG-----VPLVGLVEGGPNVSVLEVYLOEPPPIPVICDGSGRASDILSFAHKY 225
QY 265 ----ALVNO---PHLLVPVNAKOPKEKPPSKHFSMEDIVRTYTKLLQNTSHQHLTYVD 317
DB 226 CEEGGINESLREQLLV--TIKTFYNNKAQSHQFAIIMECK-----KKELVYVR 276
QY 318 FEOGSEEDVTILKALVYACKSHSOEPDYDELKLAAMRVDAIAKSEIFNGVW-- 375
DB 277 MSEGQODLEMAILTRLLKG--TNVSAP-----DQSLALANRVIDARSQIVFGHWTTP 330
QY 376 -----KSCD----- 379
DB 331 LGS LAPPTDSKATEKEKKPPMATTKGGRGKGGKKKKVKEVEEETDPRIKTELLMWNA 390
QY 380 LEEVAVDALVSNKPEFVRLFVNGADVADFLTYGRLOEIVRSVRSKSLFDLLQKQBEA 439
DB 391 LEOAMLDALVDRVDFVKLLIENGVMQHFTTPRLEELYNTRLGPPNTLHLLVDRVKS 450
QY 440 RLTLAGLGTQARBPAPPAF--SLHEYSRVLKDFLODACR-----GFYOD 484
DB 451 NL-----PPDYHISLIDIGLVLEYLGMGAYCNYTRKNFRLLYNNLFGP 494
QY 485 GRP-----GDRRAEKGPAPKPTGQKMLDLN-----OKSENWBDLFLMAVLQNR 530
DB 495 KRPKALKLGMEDDEBPAPKAKKKKKKEEIDIDVDPAVRFPQPFHELMWAVLAKR 554
QY 531 HEMATTFAMGQGVAAALAACTILKEMSHLETAA-----RATREAKERTALDLF 584
DB 555 OKNAVFLMORGESMAKALVACLYRAMAHESSESDLVDDISODLNNKDFQGLLELL 614
QY 585 SECYSSEBARAFALVRRRCMSKTCGLHATEADAKFAFDGVOAFTRIWMG--DWA 642
DB 615 DOSYKDEQIAMLKLYTELKMSNSTCLKLAVAAKRDFIAHTCSOMLTDMMMGSLRR 674
QY 643 ACTPIRLILGALCFALVTNNLITFSEEARPLRTGLEDLODLSDEKSPLYGLQGRVE 702
DB 675 KNPGLKVIWGLLPITLFLFLEPTY-----DDFSQYKSEKMEDEKKEEEN 720
QY 703 L--VAPRAQD-----RGPRAVFLTRKRWGAPVTVFLGNVMPYAFLEFLTYVL 754
DB 721 TDANADAGSRKGEENEHKKORSIPGTICCEFYNAPIVCFWYTTISYGLLLEFNVIL 780
QY 755 VDRPPOGSGPEVTLFVWFTLVLEIROGFPTEDTHLVKFTLYVGDNNKCDMYA 814
DB 781 VRM---DGNPSTLOEWIVISYSLALEKIRE-ILMSEPGLSOKIKVWLOEYNNITDVA 836
QY 815 IFLLFIVGTCRMLPSAFAE-GRITLAMDFVTLRIHIFAHKOLGPKIIVERMKOV 873
DB 837 ISTFMGAILRLQNOPMGYGRVYCVDIFWYIRVLDIFGVANKVIGPYMMMGKIMDM 896
QY 874 FFLFLFLSVLVAYGTTQALLHPRHGRLEW-IFRVLXRPYQIQIGQPLDIDARNA 932
DB 897 LYFVVMVLVLMFVGVARQILHPEE-KPSWKLARINFYMPYMIIGEVPAADID----- 950
QY 933 CSHPLLEDSPSC-----PSLYANMLVLLLVTLFVLNTVNLMLLAMS 979
DB 951 ----LYAMEINPCGENLYDEBGRILPPIPGAMLPLPAMACYLVAANIILVALLAVEN 1006
QY 980 YTFQVAVGNATWMTQORYNLIVEYHERPALAPFLLSHSLTLRRV--FKKEABHKK 1036
DB 1007 NTFEFVKSISNQWKFQRYOLIMPHDRPVLPPMIILSHIYIIMRLSRCKKXEGD 1066
QY 1037 EHLERDL-----DPLDQKVVTWETVOKENFLSKMRKRDSEGEVLKTAHAYDPLAKY 1091
DB 1067 EEBDRGKJFLSDEBELKRIHEFEQOCQOEHFRERK-EDEQOSSDERIRVTSSEVENMSM 1125
QY 1092 LGLLRBEQEK-----RIKCLSEQINYCSVLVSSVADV-----LAQGGGRSSQHG 1136

```

```

DB 1126 LEEINERETFMKTSIQVTDLRLAOLEELSNMVALENLAGIDRSDLQARS-RASSEC- 1183
QY 1137 EGSQVADHRHGIDGW 1153
DB 1184 EATYLLROSSINSADGY 1200

RESULT 7
US-09-454-854-9
; Sequence 9, Application US/09454854
; Patent No. 6316204
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
; FILE REFERENCE: 07334/004005
; CURRENT APPLICATION NUMBER: US/09/454,854
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/181,030
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 08/623,679
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-454-854-9

```

Query Match 20.2%; Score 1228.5; DB 4; Length 1533;

Best Local Similarity: 27.9%; Pred. No. 3.6e-11;

Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38;

```

QY 40 FVRVPSGAVSVLFDLLAEWHLPAPNLVSLVGEOPPAKSWLVDLRKGLVQAOST 99
DB 2 YIRVSVDTKRPDCLHLMVMDQLPRLKLLISVHGGLQHFEMQPKLYQVFGKGLIAAMTT 61
QY 100 GAWILTSALRVGLAHNQAARVDSHLASTKTVRVAAVAGMSLGLVLRRLIEAODEF- 158
DB 62 GAWITGVSTGVISHVDALKD--SSKSGRVCAIGAIWGV-----ENKEDLV 111
QY 159 ---PVHPEDDGSGPCLSDSNLSHFILVEPPGKGDGLTELRLEKHSIQ----- 211
DB 112 GKDVTIRVOTMNPSTKLSVLNNSHTHFLADNGLGKGAHVXKRLLEKHSIQKINT 171
QY 212 RAGYGTGSGIEIPVCLLVNGDPNTERISRAVEQAAPWLLIV--GSGGIADVLA----- 264
DB 172 RLGQG-----VPLVGLVEGGPNVSVLEVYLOEPPPIPVICDGSGRASDILSFAHKY 225
QY 265 ----ALVNO---PHLLVPVNAKOPKEKPPSKHFSMEDIVRTYTKLLQNTSHQHLTYVD 317
DB 226 CEEGGINESLREQLLV--TIKTFYNNKAQSHQFAIIMECK-----KKELVYVR 276
QY 318 FEOGSEEDVTILKALVYACKSHSOEPDYDELKLAAMRVDAIAKSEIFNGVW-- 375
DB 277 MSEGQODLEMAILTRLLKG--TNVSAP-----DQSLALANRVIDARSQIVFGHWTTP 330
QY 376 -----KSCD----- 379
DB 331 LGS LAPPTDSKATEKEKKPPMATTKGGRGKGGKKKKVKEVEEETDPRIKTELLMWNA 390
QY 380 LEEVAVDALVSNKPEFVRLFVNGADVADFLTYGRLOEIVRSVRSKSLFDLLQKQBEA 439
DB 391 LEOAMLDALVDRVDFVKLLIENGVMQHFTTPRLEELYNTRLGPPNTLHLLVDRVKS 450
QY 440 RLTLAGLGTQARBPAPPAF--SLHEYSRVLKDFLODACR-----GFYOD 484
DB 451 NL-----PPDYHISLIDIGLVLEYLGMGAYCNYTRKNFRLLYNNLFGP 494
QY 485 GRP-----GDRRAEKGPAPKPTGQKMLDLN-----OKSENWBDLFLMAVLQNR 530

```

```

Db      495 KRPAKLLKMGEDDEPPAKGKKKKKKKEEIDIDVDBAVSRFOYPPHELMVMAVLKMR 554
Qy      531 HEMATYFPMAGQEGVAAALAAACKIKEMSHLETEAEEA-----RATEAKYERLALDLF 584
Db      555 QKMAVFLMQGEEBMAKLLVACKLYKAMAHSESSDLDVDDISQDLNNKSKDQGLALELL 614
Qy      565 SECYSNSEARAFALLVRNRCSKTTCHLATEADAKAFPAHDGVOAFLTRIMWG--DMA 642
Db      615 DOSYGHDRQIAMKLLTYELKKNMSNSTCLKLAVAAGHRDFIAHTCSQMLTDDMMKRLMR 674
Qy      643 AGTPILRLGAFLCFALVYTNLTIFSEBAPLTGLLEDLDODLSLDEKSPLYGLQSRVEE 702
Db      675 KNPGLKVMIGILLPPTILFLEFRITY-----DDFSYQTSKENDGKKEEEN 720
Qy      703 L---VEAPRAQGD-----RGPRAVFLITRMKFGAPVYFLGAVVMYFAFLFTYVLL 754
Db      721 TDANADASGRKGDENEHKKORSIPGTCICEFNAPYKFWFYITISYGLYLLFNYYIL 780
Qy      755 VDFRPPQSGPGEVTLTFWFTVLVEIRGQFTDEDTHLVKFETLVYGDNNKCDMVA 814
Db      781 VRM---DQWPSLQEWIVISYIVSLALEKIRE--ILMSEPGKLSQKIKWMLQEWYNTIDIVA 836
Qy      815 IFLFIVGTQMLPBAFEA--GRTVLAMDPMVFTLLIHFAHKQDGPKIIVERMMKV 873
Db      837 ISTFMIGALIRLQNOPYMGYGRVICYVDIIFWYIRVLDIFGVNKYLGPRYMMIGMMIDM 896
Qy      874 FFFLFFLSVWLVAVGTTQALLPHDGRLEW--IFRRVLYRPLYQIFQOIPLDEIDEARVN 932
Db      897 LYFVIMLVLMSPGVARQAILHPEE--KPSWKLANIFPMFYMTYGEVADQID----- 950
Qy      933 CSTHPLLEDSPSC-----DGLYANMLVILLLVTLVTVLLNMLLIAMS 979
Db      951 ----LYAMEINPPCCENLYDEBGRKLPICIPGAMLTLPALMACYLLVANILLVAILAVFN 1006
Qy      960 YTFQVVOGNATPMKFORYNLIVERHERPALAPRILSHSLSTARV---FKKAENKR 1036
Db      1007 NTFEEVKISINQWVFQRIQLIMTHDRPVPRLPMLISHYIIIMRLSGRCRKKREDDQ 1066
Qy      1037 EHLERDL-----PDLQDKVVTWETVOKENFLSKMEKRRDSEGEVLRKTAHRVDFIAKY 1091
Db      1067 EBRDGLGLFLSDEBLKHLHEFEQCVQEHFREK--EDEQSSDSBRIRYTSERVNMSMR 1125
Qy      1092 LGLREDEK-----RIKLESQIYNCSVLVSVADV---LAQGGGPRSSOHCG 1136
Db      1126 LEEINERETFMKTSQTVDLRLAQLEELSRMVALLENLAGIDRSDLLQARS--RASSSC- 1183
Qy      1137 EGSQVLADHRGQIDGM 1153
Db      1184 EATYLLRQSSINSADGY 1200

RESULT 8
US-09-164-671-9
; Sequence 9, Application US/09164671A
; Patent No. 6372896
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
; FILE REFERENCE: 0734/004004
; CURRENT APPLICATION NUMBER: US/09/164,671A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: US 08/862,442
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: US 08/623,679
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-164-671-9

```

```

Query Match      20.2%; Score 1228.5; DB 4; Length 1533;
Best Local Similarity 27.9%; Pred. No. 3,6e-111;
Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38;

Qy      40 FVRVPSGAVSVLPFDLLIAEWHLPAPNLVSLVEBQDPFPAKSWLRDYLKGLVKAOST 99
Db      2 YIRVSYDTPKPDSSLHLWKMQWLEIPKLLISVHGGLQNFEMQPKLYQVFGKGLIKAMATT 61
Qy      100 GAWILTSALRGVLABHVOAQRDHSLASTSKVAVVNGMSLGRVILHRRILBEEQDEP- 158
Db      62 GAWIFTGVSSTGVISHGDALKDH---SSKSRGRCALGIAPWGVV-----EKEDLV 111
Qy      159 ---PVHYBEDDGSGQGPLCSIDNSLSHFILYVEPPPGKGDLTJELRLKHSIQO----- 211
Db      112 GKDVTRYVQTMNSPLSKLSVLMNHTHTILLADNGLTKGYAEVLRLELGHISLQKINT 171
Qy      212 RAGYGTGSIIEIPVLCILYNGDPNTERISHAEOAPMLLV--GSGGIADVLA----- 264
Db      172 RLQGG-----VPLVGLVEGSPNVVSIVLEVLOEPPPIPVICDQSGRASDILSFAPKY 225
Qy      265 ----ALVNG---PHLYPKVAEKQEKFPKSHSWEDIVYWTULONITSHOHLTYVD 317
Db      226 CEEGGIINESLREQDLV--TIQTFNNYKQAOSHQFALIMBCKM-----KKELVTVFR 276
Qy      318 FEOGSEBELDVILKALVKAACKSHQEPQDYLDLKLAVADRYDIAKSEIFNGDVEV-- 375
Db      277 MGSEGOQDIEAAILTALLKG--TVNSAP---DQSLALANRRDIARSOQLFVGCPHWTP 330
Qy      376 -----KSCD----- 379
Db      331 LGSILAPPTDSKATEKEKPPMATTKGGRGKGGKGGKVEEVEETPRKIELLMVNA 390
Qy      380 LEEYVNVALVYNNKEFPRFLFDNGADVADFLTGYRLQELVSVSRKSLLPOLLQKQSEA 439
Db      391 LEQAMLDALVDRDVFYKLLIENGVMQHFLTLIRLELNYTRLGPPNTLHLVDRVKS 450
Qy      440 RLTLAAGTQOARPPAPPAF--SLHEVSVLKDFLODACR-----GFPQD 484
Db      451 NL-----PRDHYISLIDIGLVEILMGAYRCVYTRKNFTLYNNLFGP 494
Qy      485 GRP-----GDRRAEKGPAPKPTGQKMLLDN-----QKSENPWRDLFLMAVLQNR 530
Db      495 KRPAKLLKMGEDDEPPAKGKKKKKKKEEIDIDVDBAVSRFOYPPHELMVMAVLKMR 554
Qy      531 HEMATYFPMAGQEGVAAALAAACKIKEMSHLETEAEEA-----RATEAKYERLALDLF 584
Db      555 QKMAVFLMQGEEBMAKLLVACKLYKAMAHSESSDLDVDDISQDLNNKSKDQGLALELL 614
Qy      585 SECYSNSEARAFALLVRNRCSKTTCHLATEADAKAFPAHDGVOAFLTRIMWG--DMA 642
Db      615 DOSYGHDRQIAMKLLTYELKKNMSNSTCLKLAVAAGHRDFIAHTCSQMLTDDMMKRLMR 674
Qy      643 AGTPILRLGAFLCFALVYTNLTIFSEBAPLTGLLEDLDODLSLDEKSPLYGLQSRVEE 702
Db      675 KNPGLKVMIGILLPPTILFLEFRITY-----DDFSYQTSKENDGKKEEEN 720
Qy      703 L---VEAPRAQGD-----RGPRAVFLITRMKFGAPVYFLGAVVMYFAFLFTYVLL 754
Db      721 TDANADASGRKGDENEHKKORSIPGTCICEFNAPYKFWFYITISYGLYLLFNYYIL 780
Qy      755 VDFRPPQSGPGEVTLTFWFTVLVEIRGQFTDEDTHLVKFETLVYGDNNKCDMVA 814
Db      781 VRM---DQWPSLQEWIVISYIVSLALEKIRE--ILMSEPGKLSQKIKWMLQEWYNTIDIVA 836
Qy      815 IFLFIVGTQMLPBAFEA--GRTVLAMDPMVFTLLIHFAHKQDGPKIIVERMMKV 873
Db      837 ISTFMIGALIRLQNOPYMGYGRVICYVDIIFWYIRVLDIFGVNKYLGPRYMMIGMMIDM 896
Qy      874 FFFLFFLSVWLVAVGTTQALLPHDGRLEW--IFRRVLYRPLYQIFQOIPLDEIDEARVN 932
Db      897 LYFVIMLVLMSPGVARQAILHPEE--KPSWKLANIFPMFYMTYGEVADQID----- 950

```


Db 1032 ERDGLKFLSDEBLKRLHEEBOCVQEHFREK--EDEQSSDERIRTSRVENMSRL 1090
 Qy 1093 GGLREOEK-----RIKLESQINYSVLVSSVADY-----LAQGGPRSSOHGE 1137
 Db 1091 EBNERTFPMKTSLOTVDRLAQLLELSNRMVNVALENLAGIDRSLIQARS-RASSEC-E 1148
 Qy 1138 GSQLVADHRGGIDGW 1153
 Db 1149 ATYLLROSSINSADGY 1164

RESULT 10

US-08-933-774-7
 ; Sequence 7, Application US/08933774A
 ; Patent No. 6025137
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
 ; FILE REFERENCE: 07334/004003
 ; CURRENT APPLICATION NUMBER: US/08/933,774A
 ; EARLIER FILING DATE: 1997-09-19
 ; EARLIER FILING DATE: 1996-03-29
 ; EARLIER APPLICATION NUMBER: US 08/623,679
 ; EARLIER FILING DATE: 1995-03-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 1497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-933-774-7

Query March 18.9%; Score 1150.5; DB 3; Length 1497;
 Best Local Similarity 27.4%; Pred. No. 1.8e-103;
 Matches 349; Conservative 216; Mismatches 436; Indels 275; Gaps 39;

Qy 40 FVRVPSGVAPSELPDILLAEWHLPAPNLVSLVGEBOEPFAMKSMRLDYLKGVKAAQST 99
 Db 2 YIRSYOTKPSDLHLMWKDQMLEPKLLISVHGLOLFEHQPKKQVFGKGLIKAAVTT 61
 Qy 100 GAWILTSALRVGLARHVGQAVRDSHSLASTSTKVAVVAGMASLGRVLRRLLEEAOEDF 158
 Db 62 GAWIFGTGVSIGVISHVGDALKD---SSKSRGRVCAIGIAPKGIY-----ENKELV 111
 Qy 159 ---PVHPEDDGGGQGPLCSIDSNLSHFILVEPGPGKGDGLTELRLLEHISEQ--- 211
 Db 112 GKDVTRYVQTSNPLSKLSVLNNSHTFILLDNGTLGKYGAEVLRRLLEHISLQKINT 171
 Qy 212 RAGVGTGSIETIPVLCILVNDPNTLERISRAVQOAPMWLLV---GSGGIDVLA----- 264
 Db 172 RLGGG-----VPLVGLVNBGPVNVSTIVLELQEBEPPIPVICDGGSRADILSPAHKY 225
 Qy 265 ---ALVNO---PHLVKVALEKQFKEKPSKHSWEDIIVWTKLQNTSHOHLFTYVD 317
 Db 226 CEEGGIINESIREGLLV--TIQTFNNYKAKOSHQLFALIMCMK-----KELVYFR 276
 Qy 318 PEOGSEELDTVILKALVACKSHSQEPQDYLDLKLAVANDRVIAKSEIFNGDVEM-- 375
 Db 277 MGSEGGODIEMAITLALKG--TVNSAP---DQSLALANRVDIARSOIFGVPHWTP 330
 Qy 376 -----KSCD----- 379
 Db 331 LGSIAPTDTSKATKEKKPPMAATTKGGRGKGGKGGKKEVEEETDPRIKILLNWNVA 390
 Qy 380 LEEVMDVALVSNKEEFVRLFYDNGADVADFLTYGRLOELYSVGRKSLIFDLQKOEBA 439
 Db 391 LEQMLDALVADRDPVKLLIENGVMNQHFITIRLEELVTRIGPNTLHLVDRVYKS 450
 Qy 440 RLTLAGLGTQOARPPAGPPAF--SLHEVSVLTKDFLODACR-----GFYOD 484

Db 451 NL-----PDYHISLIDIGLVEYLMGAVRCNYTRKRNFTLYNNLFGP 494
 Qy 485 GRP-----GDRRAEKGPAPKPTGQKMLLDLN-----QKSENPRDLFLNAVLONR 530
 Db 495 KRPKALLLGMEDEDEPPAKGKKKKKKKEEIDIDVDPAVSRRQYFPHELMAVAVLMKR 554
 Qy 531 HEMATYFWANGQEGVAAALAACTILKEMSHLETEAANA-----RATREAKERYLALDLF 584
 Db 555 QKMAVFLMORGEESEMAKALVACKLYKAMAHESSESDLVDDISQDLDNNSKDFGLALELL 614
 Qy 585 SECNSNEARAFALLVNRNCWSTKTGLHATEADAFAFFHDDVOAFLTYMNG--DMA 642
 Db 615 DQSYKHDEQIAMKLLTYELKNWSNSTCLKLAVAKHDFIAHTCSQMLTMMNGRLMR 674
 Qy 643 AGTFLRLLAGFLCFALVYTNLTITFSEEARPLRTGLELDLODLSLDTESPLYGOSRYEE 702
 Db 675 KNPKLXYIMGLLPLPTLIFLEFRY-----DFSTQTSKENDGKEEEN 720
 Qy 703 L---VEAPRAQD-----RGRAVFLLTRMKFGAVTVFLGNVNYFAFLPFTYVL 754
 Db 721 TDANADAGSRKGDENEHKKQRIPIGTKICKFNADIVKFWFTISIGVLLFNVTYL 780
 Qy 755 VDFRPPQGSBPVTYTFVNVFTVLEIRQGFPTDETHLYKFTLYGDNMKCDMVA 814
 Db 781 VRM---DQWPSLOEMIVISYIVSLALEKIRE-ILMSEPGKLSQKIKYVLOEYNNITDLVA 836
 Qy 815 IFLFIVGTCRMLPSAFEAGRTVLAQPMVFTLRLHIHPIHQLGPKIIVESMMKQVF 874
 Db 837 ISTWIGAM-----ATRSVM-----MIGKMMIDML 861
 Qy 875 FFLFELSVLWAVGVTTQALLPHDGRLEW-IFRRVLYRPLQIFGOIPLDEIDEARVNC 933
 Db 862 YFVIVMLVVLMSFCVAAQALHPEE-KPSWKLANIIFYMPWMLYGEVPAQDID----- 914
 Qy 934 STPELLEDSBSC-----BSLYANMVLILLTFLLVTVNLMLLIAMFSY 980
 Db 915 ---LYAMEINPPCGENLYDEBCKRLPFCIGAMCTPALMCYLLVANILLVNLIAVFN 971
 Qy 981 TFOVQGNATMFMKFORVYNIIVEYHERPALAPRILLSHLSLTLRV---FKKAEHRE 1037
 Db 972 TFEVKSISQWVKFYQYQLMTFHDRPLPPMTILSHYITIIWLRSGCRKRKEGDE 1031
 Qy 1038 HLERDL-----PPLDQKVVTWETVQKENFLSKMEKRRDSEGEVLKRTAHRVDIAKYL 1092
 Db 1032 ERDGLKFLSDEBLKRLHEEBOCVQEHFREK--EDEQSSDERIRTSRVENMSRL 1090
 Qy 1093 GGLREOEK-----RIKLESQINYSVLVSSVADY-----LAQGGPRSSOHGE 1137
 Db 1091 EBNERTFPMKTSLOTVDRLAQLLELSNRMVNVALENLAGIDRSLIQARS-RASSEC-E 1148
 Qy 1138 GSQLVADHRGGIDGW 1153
 Db 1149 ATYLLROSSINSADGY 1164

RESULT 11

US-09-181-030-7
 ; Sequence 7, Application US/09181030
 ; Patent No. 6251597
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
 ; FILE REFERENCE: 07334/004005
 ; CURRENT APPLICATION NUMBER: US/09/181,030
 ; EARLIER FILING DATE: 1998-10-27
 ; EARLIER APPLICATION NUMBER: US 08/862,442
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: US 08/623,679
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7


```

QY 318 FEQGSSELDVILKALYKACKSHQEPQDYLDELKLAAMDRAVDIAKSEIFNGDVEW-- 375
DB 277 MGSEGOQDIEMALITLALKG--TNVSAP---DQSLALANRVDIAKSQIFVGPBHTP 330
QY 376 -----KSCD----- 379
DB 331 LGSILAPPTDSKATEKEKPRMATTKGGRGKGGKGGKKEVEEBETDPKRIELLMVNA 390
QY 380 LEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYRSVRKSLFDLORKOBEA 439
DB 391 LEQAMLDALVDRVDFVLLIENGVMQHFLLTIPRLEELYNTRLRPPTLLHLVADVKS 450
QY 440 RLTLAAGTQOARBPAPPAF--SLHEVSRVLKDFLODAGR-----GFYOD 484
DB 451 NL-----PDYHISLIDIGLVEYLMGAVRCNTRKNFRTLYNNLPGP 494
QY 485 GRP-----GDRRAEKGPAPKPTGQKMLLDN-----OKSENPMRDLFLMVLQNR 530
DB 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEIDIDVDPAVSRFQYPPELHMVMAVLMKR 554
QY 531 HEMATYFWAMGOEGVAAALAACTIKEMSHLETEAEEA-----RATREAKYERLALDLF 584
DB 555 OKMAVFLMORGEESMAKALVACKLYKAMAHSSSDLDVDDISODLDNNSKQFGOLATEL 614
QY 585 SECYNSSEARAFALLVRRRCWSKTTCLHATEADAKAFPAHDGVOAFLTRIIMG--DMA 642
DB 615 DOSYHDSQIAMKLLTYELKQNSNSTCLKLAVAAGHROFIANTCSQMLTDMNGRLMR 674
QY 643 AGTPLRLGALFCALVYTNLITSEAPLRTGLDLODLSLDTESPLYGOSRVEE 702
DB 675 KNPGIKLVGILPITLIFLEERTY-----DPSYOTSENEDEKKEEEN 720
QY 703 L---VEAPRAQD-----RGPRVFLTRMRKMGAPVPLGVNVVMAFLFETLYVL 754
DB 721 TDANADASRKGBDENEHKQRIIPITGICKFVAPVYKPFYITISLUGVLLFNYYL 780
QY 755 VDFRPPQSGPEVTLVFWVFTLVLEIRQGFPTDEBTHLVKKEFTLVYGDNMKCDWA 814
DB 781 VRM---DQMPSLQEWIVISIVSLALEKRE--LMSPEGKLSQKIKWMLQEWMTITDLVA 836
QY 815 IFLFVGTVCMLBSAFEAGRTVLADENVFTLRLLIHFAHKQUGPKIIVERMKDVF 874
DB 837 ISTFMIGAM-----ATRSVM-----MIGKWMIDL 861
QY 875 FFLFPLSLVAVYVTTQALLHPHQRLEW--IFRVLVIRPVIQIGQIPBDEIDARVNC 933
DB 862 YFVVMVLVMSFGVARQALHPBE--KPSWKLARNIFVMPYMWIYGEVFAQDID----- 914
QY 934 STHPLLEDSPSC-----PSLYANMLVILLVPLVTLVTLNMLLJAMFSY 980
DB 915 ---LYAMEINPPCGENLVDEBGRKLRPCIPGAMVLPALMACYLLVANNILLVNLIAVERN 971
QY 981 TPQOVQGNATMFWKFORYNLIVEYHERPALADPFIILSHLSTLLRV---FKKEAHEKRE 1037
DB 972 TEFPEVKSISNQWKFORYOLIMTFPHDRPVLPPMILISHIYIIMRLSGRCKKEGDOE 1031
QY 1038 HLERL-----PDPDQKVVTWETVQKENFLSKMKERRRDSGEVLRKTAHVVDIATKL 1092
DB 1032 ERDRCLKFLSDEELKRLHFEEOCVQEHFKEK--BDEQOSSSDERIRVTSSEVENMSRL 1090
QY 1093 GGLREQEK-----RIKLESQINVCVLSVAVDV---LAOGGGRSSQHGCE 1137
DB 1091 BEINRETFPMKTSLOTVDRLRLAQLEELSNRMNALENLAGIDRSLQARS--RASSEC-E 1148
QY 1138 GSQVLVADHRRGIGDM 1153
DB 1149 ATYLLRQSSINSADGY 1164

```

RESULT 13
US-09-454-854-7
Sequence 7, Application US/09454854

```

; Patent No. 6316204
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
; FILE REFERENCE: 07334/004005
; CURRENT APPLICATION NUMBER: US/09/454, 854
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/181, 030
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 08/623, 679
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-454-854-7

Query Match      18.9%; Score 1150.5; DB 4; Length 1497;
Best Local Similarity 27.4%; Pred. No. 1.8e-103;
Matches 349; Conservative 216; Mismatches 436; Indels 275; Gaps 39;

QY 40 FVRVPSGVAPEVLDLLAEWHLPAPNLVSLVGEBOFPANKSWLRDYLKGLVYQAOST 99
DB 2 YIRSYDTRKPSLSLHWKQWLELPKLLISVHGLONFEMQPKLVQVFGGLKAAWTT 61
QY 100 GAWILTSALRYGLARHQAVRDSLASTSTKRVAVAGMASLGRVLRRLLEBAQEDF- 158
DB 62 GAWIFGTGVSSTVSHVDALKDH---SSKSRGVCAIGIAPWGIIV-----ENKEDLV 111
QY 159 ---PVHYPEDDGGSGPFLCSLDSNLSHFILYEPGPQGDGLTELRLEKHSRO----- 211
DB 112 GKDVTRYVQYTNMSPKLSVJLNSHTFILLDNGTLGKYGAEVKRLRLEHGISLQKINT 171
QY 212 RAGYGTGSIPIPVLCVLVNGDPNTERISRABVOAEMVLLV--GSGGIADVLA----- 264
DB 172 RLQGG-----VPLVGLVVEGGPVVSVILEYLDPEPPIPVICDSSGRASDILSPAKY 225
QY 265 ---ALVNO---PHLYPKVAEKQKPEKPSKFSMEDIVRWTKLONITSHQHLTYD 317
DB 226 CEEGIIINESIREOLLV--TIQTFNVYKQASHOLFALIMECK-----KKELVTVFR 276
QY 318 FEQGSSELDVILKALYKACKSHQEPQDYLDELKLAAMDRAVDIAKSEIFNGDVEW-- 375
DB 277 MGSEGOQDIEMALITLALKG--TNVSAP---DQSLALANRVDIAKSQIFVGPBHTP 330
QY 376 -----KSCD----- 379
DB 331 LGSILAPPTDSKATEKEKPRMATTKGGRGKGGKGGKKEVEEBETDPKRIELLMVNA 390
QY 380 LEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYRSVRKSLFDLORKOBEA 439
DB 391 LEQAMLDALVDRVDFVLLIENGVMQHFLLTIPRLEELYNTRLRPPTLLHLVADVKS 450
QY 440 RLTLAAGTQOARBPAPPAF--SLHEVSRVLKDFLODAGR-----GFYOD 484
DB 451 NL-----PDYHISLIDIGLVEYLMGAVRCNTRKNFRTLYNNLPGP 494
QY 485 GRP-----GDRRAEKGPAPKPTGQKMLLDN-----OKSENPMRDLFLMVLQNR 530
DB 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEIDIDVDPAVSRFQYPPELHMVMAVLMKR 554
QY 531 HEMATYFWAMGOEGVAAALAACTIKEMSHLETEAEEA-----RATREAKYERLALDLF 584
DB 555 OKMAVFLMORGEESMAKALVACKLYKAMAHSSSDLDVDDISODLDNNSKQFGOLATEL 614
QY 585 SECYNSSEARAFALLVRRRCWSKTTCLHATEADAKAFPAHDGVOAFLTRIIMG--DMA 642
DB 615 DOSYHDSQIAMKLLTYELKQNSNSTCLKLAVAAGHROFIANTCSQMLTDMNGRLMR 674
QY 643 AGTPLRLGALFCALVYTNLITSEAPLRTGLDLODLSLDTESPLYGOSRVEE 702

```

```

Db      675 KNPGLKVMIGLLPILFLEFRTY-----DPSYQTSKXENEDGKEEBEN 720
Qy      703 L---VEAPRAQD-----RGPRAVFLTRMKFKMGAPVTVFIGNVMYFAFLFTLYULL 754
Db      721 TDANDAGSRKGDDENEHKORIIPIGTICKCFYNAPIVKFWFYTISYLGYLILFNYVIL 780
Qy      755 VDFRPPQSGPEVTLVFWFTLVLEIRIOGFDEDETHLVKKFTLVYGDWNNKCDMVA 814
Db      781 VAM---DGMPSLOEWIVISYISLAEKIRE-ILMSEBGLSOKIKWMLQEWNTITDLVA 836
Qy      815 IFLFIVGTCTMLPSAFEGARTVLAMDPMFTLRILHFAHKOLGPKIIVERMKDVF 874
Db      837 ISTFMIGAM-----ATRSVM-----MICKWIMDL 861
Qy      875 FFLFLSLWLVAVGYTTQALLPHDGRLEW-IFRRVLYRPYQIQRQIPLDIDEARVNC 933
Db      863 YFVVIMLVLMISFGVARQAIHPHE-KPSMKLARNIFMPYMWIYGEVADQID----- 914
Qy      934 STHPILLEDSPSC-----PSLYANMLVILLVTLFVLVTNVLNMLLJAMFSY 980
Db      915 ---LYAMEINPPCGENLYDEBGRKLPCTPGAMLTALMACYLLVANILLVNLLAVERN 971
Qy      981 TFOVVOGNATMFKFORVNLIVEYHERPALAPFILLSHLSLTLRRV---FKKEAHEKRE 1037
Db      972 TFEVKSISNQWKKFORQOLIMTPHDRVLPPLMIISHIYIIMRLSGCRKKEGDOE 1031
Qy      1038 HLERDL-----PDPLDQKVVTWETVOKENFLSKMEKRRDSEGEVLRTAHVDFIATKL 1092
Db      1032 ERDRGLKFLSDEELKRLHEFEQCQVQHFREK-EDBOOSSDERIRVTSERVENMSML 1090
Qy      1093 GGLREOEK-----RIKLESQIYVCSLVSSVADV---LAOGGPRSSOHCGE 1137
Db      1091 E1NERETETKTSLOTVDRLOLELSNRMALENLAGIDRSLLQARS-RASSEC-E 1148
Qy      1138 GSQVAAADHRGGIDGW 1153
Db      1149 ATYLLRQSSINSADGV 1164

RESULT 14
US-09-164-671-7
; Sequence 7, Application US/09164671A
; Patent No. 6372896
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; FILE REFERENCE: 07334/004004
; CURRENT APPLICATION NUMBER: US/09/164,671A
; EARLIER APPLICATION NUMBER: US 08/862,442
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: US 08/623,679
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1497
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-164-671-7

Query Match      18.9%; Score 1150.5; DB 4; Length 1497;
Best Local Similarity 27.4%; Pred. No. 1,8e-103;
Matches 349; Conservative 216; Mismatches 436; Indels 275; Gaps 39;

```

```

Db      62 GAMIFTGSTGVISHVDAIKDH---SSKSRGRVCAIGAPWGIV-----ENKEDLV 111
Qy      159 ---PVHYEDDGGSGGCPCLSDNSLHPIVPEPPGKGGDGLTELRLLEKHSIQO----- 211
Db      112 GKDVTRVYQTMSPNPSKLSVLNNSHTHFLIDNGTLGKGAEVKLRLLEKHSIQOKINT 171
Qy      212 RAGYGTGSIIEIPVLCILVNDPNTLERISRAVEQAMWILV--GSGGIADVLA----- 264
Db      112 RLQGG-----VPLGLVVEGGPNVSVILEYLOEERPIPVICDGSGRASDIISFAKY 225
Qy      265 ---ALVNO---PHILVPAVEKQKFKPSPKSHSEDIYKWTLLQNTSHQHLTYVD 317
Db      226 CEEGGIINESREQLV--TIQKTFNNYKAOSHOFATIMCMK-----KKELVTFR 276
Qy      318 FEOGSEELDTVILKALVAKCKSHSOEPODYDELKLVANDRVDIKSEIFNGDVEN-- 375
Db      277 MGSEGOODIEALITALLKG--TNVSAP---DQLSLANRRVDIASQIFVGPHPHTP 330
Qy      376 -----KSCD----- 379
Db      331 LGS LAPPTDSKATEKEKKRPMAATTGKRGKGGKGGKGYKEEVEDTDPRKIETLNMVNA 390
Qy      380 LEEVWVDAVLSNKEPEFVFLVNDGADVADFLTYGLOLYRSVSKSLPDLLOKQOSEA 439
Db      331 LEQAMLDALVIDRVDFVFKLLIENGVMQHFLLTPELBELVYTRIGRPNTLHLVADVKS 450
Qy      440 RLLTAGLGTOQAREBPAPAF--SLHEVSRLKFLQDACR-----GFYOD 484
Db      451 NL-----PDYHISLIDIGVLEYELMGATRCNTRKGRFTLYNNLFGP 494
Qy      485 GRP-----GDRRAEKGPAPKPTGQKMLDLN-----OKSENPWRDLFMAVLONR 530
Db      495 KRPKALKULGMEDEDEPPAKGKKKKKKKEEIDIVDDPAVSFPQYPHELMVMAVLMKR 554
Qy      531 HEMATYFPAQGOEGVAAALAAACKILIKENSHLETEBA-----RATEAKYERLALDLF 584
Db      555 QMAVFLWQGBESMAKALVACKLYKAMAHESSEDLVDDISQDDINNSKDFGQALABEL 614
Qy      585 SECYNSERAPFALLVRNRCSKTTGHLATEADAKAFPAHDQVQAFLTRIMWG--DMA 642
Db      615 DQSYHDIQIAMKLLTYELKWNNSSTCLKLVAAHGRPFIAHTCGMLITDMKRLMR 674
Qy      643 AGTPILRLGAFLCFALVYTNLIJFSEBAPARTGLEDLODLSLDTESPLYGLOSRAVEE 702
Db      675 KNPGLKVMIGLLPILFLEFRTY-----DPSYQTSKXENEDGKEEBEN 720
Qy      703 L---VEAPRAQD-----RGPRAVFLTRMKFKMGAPVTVFIGNVMYFAFLFTLYULL 754
Db      721 TDANDAGSRKGDDENEHKORIIPIGTICKCFYNAPIVKFWFYTISYLGYLILFNYVIL 780
Qy      755 VDFRPPQSGPEVTLVFWFTLVLEIRIOGFDEDETHLVKKFTLVYGDWNNKCDMVA 814
Db      781 VAM---DGMPSLOEWIVISYISLAEKIRE-ILMSEBGLSOKIKWMLQEWNTITDLVA 836
Qy      815 IFLFIVGTCTMLPSAFEGARTVLAMDPMFTLRILHFAHKOLGPKIIVERMKDVF 874
Db      837 ISTFMIGAM-----ATRSVM-----MICKWIMDL 861
Qy      875 FFLFLSLWLVAVGYTTQALLPHDGRLEW-IFRRVLYRPYQIQRQIPLDIDEARVNC 933
Db      863 YFVVIMLVLMISFGVARQAIHPHE-KPSMKLARNIFMPYMWIYGEVADQID----- 914
Qy      934 STHPILLEDSPSC-----PSLYANMLVILLVTLFVLVTNVLNMLLJAMFSY 980
Db      915 ---LYAMEINPPCGENLYDEBGRKLPCTPGAMLTALMACYLLVANILLVNLLAVERN 971
Qy      981 TFOVVOGNATMFKFORVNLIVEYHERPALAPFILLSHLSLTLRRV---FKKEAHEKRE 1037
Db      972 TFEVKSISNQWKKFORQOLIMTPHDRVLPPLMIISHIYIIMRLSGCRKKEGDOE 1031
Qy      1038 HLERDL-----PDPLDQKVVTWETVOKENFLSKMEKRRDSEGEVLRTAHVDFIATKL 1092
Db      1032 ERDRGLKFLSDEELKRLHEFEQCQVQHFREK-EDBOOSSDERIRVTSERVENMSML 1090

```

Qy 1093 GGLAEQEK-----RIKLESQINYSVLVSVADV----LAQGGGRSSQHCE 1137
Db 1091 EEINEREFEMKTSLOTVDRLAQLEBELSRMVNALENLAGIDRSLIDARS- RASSEC-E 1148
Qy 1138 GSQVLAADHRCIDGM 1153
Db 1149 ATYLLRQSSINSADGY 1164

RESULT 15

US-09-020-956-112
; Sequence 112, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-112

Query Match 13.3%; Score 813; DB 3; Length 315;
Best Local Similarity 52.4%; Pred. No. 2.3e-71;
Matches 162; Conservative 53; Mismatches 68; Indels 26; Gaps 5;

Qy 843 MFTFLRLHIFPAIHKOLGKTIIVERMMKDVFFFLPFLSVMLVAGVTTQALLHPDGR 902
Db 1 MFTVRLHIFVNLKOLGPKIVISKMKDVFFFLPFLGVLVAGVATEGLRPRDSDF 60
Qy 903 EMIFRRVLVRYPLQIFGOIPLEIDEARV---NCSTHPLLEDSP-----SCPSLYANWL 954
Db 61 PSILARVRYRPLQIFGOIPQEDMDVALMEHNSCSSEPFMAHPGAQAGTCSQYANWL 120
Qy 955 VILLIVTLVTLVNLVLLIMFSTYTPQVVOGNATMFWKFORYNLIYVYHERPALADPF 1014
Db 121 VLLIVIFLVNLVNLVLLIMFSTYTPGKVQGNSDLYKQRYRLIREFHSRPAADPF 180
Qy 1015 ILLSHLSLTIRRVFK-----EASHKREHLERDLDPIDQKVMTMETVQKENFLSK 1065
Db 181 IVISHRLRLRLKOLCRPNPSPQSSPALHFRVYLSKE---AERKLTWESVYKFNFLLA 236

Qy 1066 MEKRRDSEGEVLKRTAHVDFIAKYIGLREQEKRIKLESQINYSVLVSVADVIAQ 1125
Db 237 RARDKRESDSERLKRSTOKVDLALKOLGHIREFYQRLKVLIEREVQOCSRVLGWVAEALSR 296
Qy 1126 G-----GGP 1129
Db 297 SALLPFGGP 305

Search completed: September 10, 2003, 09:42:29
Job time : 27 secs

THIS PAGE BLANK (USPTO)

0y	307	T---	SHOHLTYVDEBQSGSEBTDVILKALVYACKSHSQSEQVLDLDEKXAVANDRDI	363
Db	489	TVCAQHKLTLTIFRLQEGEHVDHAILTALKG----	QWLSAADQJALALANNRVDI	542
0y	364	AKSEIFNDVEMKSCDLEEVNDAIVSNKPEFVFLVNGADVADFLTGYRLOEY----		419
Db	543	ARSDVFAAGHEMPQALANNAMEALIHBRVDFVRLLEQGINMQFVLTISRDELXYNDK	602	
0y	420	-----RSVSRK-----	SLLEPDL-----	ORQSEARL- 441
Db	603	GPENLTXYIVDVVAVRQGYRFLKPDIGLVIETKMGNSYQCSYTTSEPRDKYKQMKRYK	662	
0y	442	-----	TLAGLCTOQAR-----	PPAGPRA-F 461
Db	663	HAOKKAMGVFSSRPSRTSGIASRSTGCMGVGSSVAGVFGNSFGNODPELDPHVR	722	
0y	462	SLHEYSRVLQPEL---QDAGRFGYQDGRGDRRAEKGAKPRTGQKMLDLINQSEN---	516	
Db	723	SALSGSRLLSNHILMRSAPRGVNF----	PANPMRPNLGDSDRCGSEFPBEELSTISASGCS	778
0y	517	-----	PWBDLFMAVLQNRHEMATYFWAMQBGVAALAAACKILKEMS-----	HLE 562
Db	779	QTEPDRFRPYSELMLMVAULTKRODMAMCMQGEAMAKALVACRLYXSIASTEADYLE	838	
0y	563	TEABARAATREAKTERLALDFSECSYNSSEARAFALVRRNCWSKTTCLHATEADAKA	622	
Db	839	VEICEELKKVAAEEFRLLSELELDHCYHADDQTLTLLTYELSNMNETCLAVIVNNKH	898	
0y	623	FPANHGVAQFLTRIMWGMAAGT-PIILULGAFLOFPAV-----		660
Db	899	FLAHCCOILADLHGGRLMRKTHSNIKVGLICPPLOMLBFTREBLLNQOTAAEH	958	
0y	661	-----	YTLITFSEEARPLRTGLEDDQDIDSIDTE-----	689
Db	959	QNDNMVSSSSSSSSSSSSSSSSSSSSSPEDDDENNANHNDQKTRKTSQSGASLNTS	1018	
0y	690	-----		689
Db	1019	LPHSRRRKAKKNEKCDRETDASACEAGNRQIONGLTAEGTFGEHNGSVPPPYMRANS	1078	
0y	690	-----	XSPLYGLOSREVELVAPRAQDR-----	GPAVFLTLTWKRFW 728
Db	1079	RSRYNRRSDMSKTSSVITGSDPNLSKLOQSNTSTDRPNMEQFOGTIKIKRRRFYFY	1138	
0y	729	GAPVTFVFGNVVMAEAFILFTYVLLVDFRPPQSGSEPVLYVWVFTLVLEEIRQGF	788	
Db	1139	SAPISTFMSWISITFLITFTFTYLLV--KTPRR-PLYIEYLLIYVAAFGLEGYRKIIM	1199	
0y	789	TDEBTHLVKFTLVYGDNNKCDMAVILFLVIGVTCRMLPSAFAEGRTVLAMDFWFLR	848	
Db	1196	SDAKP-FYEKIRTYVCSFWNCVTILAIIFYIYGFMRCEFSV-AVGRVILACDSVLTMTK	1253	
0y	849	LHIFAIHKOLGPKTIIVERMKKVDFFLFLSTVWLVAVGYTQALLPHDGRLEWIF-R	907	
Db	1254	LLDVMSVHPKIGPYVTAGMKMIQNNSYIIMLVLTLSFGIAROSITYP-DETWMIILVR	1312	
0y	908	RVLYRYPQIQOGLDEIDEARVNCSTH-----	PLLEBSP---SCPSLYANML	954
Db	1313	NIFLKPYPMLGVEVADEID----	TCGBANDQHLENGEPVILGNTTGSLCVPEY--	WI 1366
0y	955	VILLVTLVFLVNVVLLMNLMIAMFSYTFQVVGNAITWFKFORYNLIYEHERRPALAEP	1014	
Db	1367	PPLMTFFLLANILMLMMLAIIFNHIIFDADTEMGQIMLFORXYQVMEVSTPLPPL	1426	
0y	1015	ILLSHLSTLRVFKKEAEKREH-----	LERDLPDLQCVVTVWYQKENFL-S	1066
Db	1427	TPLYHGVLITQFVTRFLSCSQSEBNPILLLKIALFLFDNOQIEKLHFEEDCMEIDLARQ	1486	
0y	1065	KMEKRRRDSBEGVLEKTAHR-----	VDLIAKYLG---LRQEKRIKLESQINYSV	1114
Db	1487	KLNEKNTSNEORILADIRTDQILNRLDLOKQESMGDVINDVSRILASVEKAON--E	1543	

RESULT 2
T22644

hypothetical protein F54D1.5 - Caenorhabditis elegans
CISpecies: Caenorhabditis elegans
CDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CAccession: T22644
R:Lennard, N.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19592

A:Accession: T22644
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1400 <MIL>
A:Cross-references: EMBL:Z77132; PIDN: CAB00861.1; GSPDB: GN00022; CESP: F54D1.5
A:Experimental source: clone F54D1
A:Genetic8:
A:Gene: CESP:F54D1.5
A:Map position: 4
A:Introns: 21/2; 51/2; 205/2; 276/3; 364/2; 394/2; 466/3; 507/3; 536/3; 599/3; 672/2; 692/2

Query Match 16.3% Score 990; DB 2; Length 1400;
Best Local Similarity 27.7%; Pred. No. 3.4e-63;
Matches 334; Conservative 202; Mismatches 401; Indels 188; Gaps 46;

Db 151 GTIVFGGGAHAKAQVYRLSYDSEPLDMYLMEKWLGPRLVITVHGGMNFELERL 210
QY GEVNF-GSGCKRGKFVRVPAGVAPSVLPDLLAEWHLPAFNLVSLVGSEOPAFMKSWL 84
Db 151 GTIVFGGGAHAKAQVYRLSYDSEPLDMYLMEKWLGPRLVITVHGGMNFELERL 210
QY 85 RDVLRKGLVRAAGSTGWMLTSLARVGLAHVGVADHDLSASTSKRVRYAVAGMSLGR 144
Db 211 GLRLRRKKMLKAQTGGAMITTSGLDSGVHVAAAL--DEAGISARKMSQITVTIGIAPGV 269
QY 145 VLHRIILEAOEDPPVHYREDGSGGPLCSLDNSLSHFLIVEGPRPGKDGLTELRL 204
Db 270 IKKERILLRONEH--VYYDVHSLSVNMANGINDRHSHYFLIADNGTVGRGADLHLRQL 327
QY 205 EKHI SEOPAGYGSTGEIEIPVLCLLVNGDPNTLERISRAY--EQAAPWLLVSGGIADV 262
Db 328 ENHI-----ATGCGNGR-KVPVCTLLLEGGSISSIAIHIDVYTMKPDIPAIVCDGSGRAADI 382
QY 263 L---AALVNQHLLVPRVAEK---QEKEKPSKHFSDIVRMTKLIQNTSHQHLLTY 316
Db 383 ISPARAYINSDGTFAAVEGERLNLIKMPPEP--DOENFR-KITECVI-RDDLIRIF 437
QY 317 DPEQGESELDTVLILKLVACKSHSQEPDYDELKLAAAMPBVDIAKSEIFNGVEWK 376
Db 438 RYGOEEBEDVDVILSTVLQ----KNLPPD--EQALLTLISMNRVDLAKSCLFSNGKWS 491
QY 377 SCDLIEVMDALVSNNKEPFVRLFYVNDGADVAADFLTTCRLOELY-----RSYSKASLL 428
Db 492 SDVLEKAMNDDLYMDRVDFVECLLENGVSMKNFESISIRLENYLMDDINSASHSVRNMMEN 551
QY 429 FDLLQRQOEARKLLTAGLGTOQAAREPPAGPASFHSHEVSVLKDPLDACRGFYQDGRPG 488
Db 552 FDSM--DPHTYLLTPMIG-QOVEKLMG-NAPFLYTTSRSFK-----GKYD 592
QY 489 DRRRAEKGP--ARRPTGQKWLL-----DLNQKSEN-----PWBDLFMAVLONHEM 533
Db 593 RYKRIINGSSYHRKRKIYQKELPKKSSDDQINDNEEDSFSAFYFDNLLIMAVLTSHG 652
QY 534 ATYWAMQGECVAAAALAACKIKL-----EMSHLETAEARATREK-KTERLALDFS 586
Db 653 AECMWVAGEBDMAKCLAIRLYKATAKTIADEVIDV-EAKRFIDNVAKCREDAIBELDQ 711
QY 587 CYNSEBARFALIVRRRCWSKTTCHLATEADAKAFAPADVGQAFTRIMWGDM--AAG 644
Db 712 CYRADHRTLRLEMLPHWGNNNCLSLAVLANKTFTLAPPCOIIILAELMHSGSLKVRSG 771

QY 645 TPILRLGAFIC-----PALV-----TNLITFSEBAPLRTGLEDI--ODLSLDTEKSPLY 694
 Db 772 SNV--RVLTALICPPALIFMAVKPKSKTARLLSEETP-----EQLPYRESISTSTSNRY 825
 QY 695 GLQGRVEELVEAPRAQG-----DGRPAVF-----LITTRRK 726
 Db 826 RYSGPPEQKTLLEKGSYTKKVTIISRKNSGVASVGSASSMFKPEPOLNKKERRA 885
 QY 727 FPGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPGSGREVTLTFWVFTLVLEIRG 786
 Db 886 FYSSPITFMSWCIAFLIFTTCIILFE---TSKSKYEMITFIYTVLSVHIRK- 941
 QY 787 FTDEDTHLVKKFTLVYGDNNKCDMAIFLFTVGTCTMLPSAFEA--GRTVLAMDWF 845
 Db 942 LMTSEGSINERKVKFYAKWYNITSAALLFLVGYGFLVPMYRHSNGRVLSFSNVLF 1001
 QY 846 TLRILHFAIKQCPKIIIVERMMKDVFFFLFSLVWLVAYGTTQALLPHRGRLEWI 905
 Db 1002 YMKTFEYLVHPPLGPIYQMAKAVMSVCYICVLLVPLMAFGVNRQALTEPNYKDWML 1061
 QY 906 F-RRLVLRPYLQIFGOIPLDEIDEARVNCSTHPLLEDSPCPSLYANWLVILLVFL 964
 Db 1062 LVRLIFKPYFMYLGEVYAGEID-----TCG-----DEGICFPGY--FIRPLMVFIL 1109
 QY 965 VTNVLNMLLIAMFSYTFQVVGNAFMFKQRYNLIVYHERPALAPFILLSHL---- 1020
 Db 1110 VANILLNLLIAIFNNIYVDSIEKSEIMLFQRYQOLMEYHDSPLPFPFISFAHVHFI 1169
 QY 1021 --SLTLRVRFK-----EAHNR--EHLERLPPLOKVTWTVOKEPFLS 1064
 Db 1170 DYLVNLRPDKRRPSEHSIKLSTVEDMKRIQDFEEDCIDTLTR-----IRK---L 1218
 QY 1065 KMEKRRDSEGEVLRTAHRY-----DFIAKYLGLREGEKRIKCLESOINYSVLVSS 1118
 Db 1219 KLVNKEPLSVDTLDELTCQRVHDMQENFLK-----SRVYDIETKIDHISNSDE 1269
 QY 1119 VADV 1123
 Db 1270 VVGIL 1274
 RESULT 3
 T18951
 hypochetrical protein C05C12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18951
 R:White, S.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19050
 A:Accession: T18951
 A:Molecule type: DNA
 A:Releides: 1-1707 <ML>
 A:Cross-references: EMBL:Z68333; PIDN:CAA92726.1; GSPDB:GN00022; CESP:C05C12.3
 A:Experimental source: clone C05C12
 C:Genetics:
 A:Gene: CESP:C05C12.3
 A:Map position: 4
 A:Intons: 13/3; 52/3; 82/3; 100/3; 174/3; 203/1; 249/2; 292/1; 358/2; 406/2; 436/2; 477/2
 542/3; 1595/1; 1647/2; 1673/3; 1695/3
 Query March 14.5%; Score 881; DB 2; Length 1707;
 Best Local Similarity 22.2%; Pred. No.3.8e-55;
 Matches 306; Conservative 227; Mismatches 465; Indels 380; Gaps 41;

QY 146 LHRRIIEAOEDFVHYPEDDGSQGPLCSLDSNLSHFILVEPPEKGDGLTELRLLE 205
 Db 314 KQRS--RFVGKDSVTYATVFNNT--RLKELNDHSHFLPSDNTVRYGAEIIMRRBLE 370
 QY 206 KHISEQAGYGGTGSIIIPVLCILVNDPNTLERISPAVE--QAAPVLIVGSGIADVL 263
 Db 371 AYLAQ-----GDKRSALPLVCVLEGAFTIKVHVYVTTI PRIPIVYICGSGRADIL 425
 QY 264 A-----ALVNPPLLV---PVAEKQREKRPKSHGFSMEDLVRTKL 302
 Db 426 AFAHQAVSNGFLSDNIRNQLVNIVRRI FGYPPTAKLILKQ----- 467
 QY 303 LQNTSHQHLITVYDFQESSELDVTILKALYKACSHSOEPQDYLDELKAVAMPVD 362
 Db 468 IVEGNTKSLMTIFRLQESSREDIDHYMCL---KQMLSPF---EQQLALANMRAD 521
 QY 363 IAKSEIFNGDVWKSCDLEEVMDALVSNKPEPVRLFVNDGADVADFLTYGRLOELY-- 419
 Db 522 IARTEIPANGTEWTTQDLNHNAMTEALSNDRIDFVHLLLENGVSMQFLTYSRLEHLYNTD 581
 QY 420 ---RSVRSKSLPDLQKQBEARLTLAGTQOAREPPAPRAFSLHYSRVKDFLOD 476
 Db 582 KGPQNTLRNLVDSKH-----IKLVEGRIVENLMGN 615
 QY 477 ACRGFYOD-----GRPDRRRAEK----- 495
 Db 616 LYKSNYTKFEKQYFLFNRRKQGRKRVHNSNGRNDVIGSPSDAGREKMSQISLIN 675
 QY 496 -----GPAKPTQOKMLLDNOKSEN-----PWRDLFLMAYLONHEMATY 536
 Db 676 NARSIISLFGNGGRKREDEDDFSLNEEAMNDFPRYPYSDLMIAVLTKQOKAKL 735
 QY 537 FPMAGCGVAAALAAKILKEMSHLTEAPAAATRA-----KYERLALDFS 585
 Db 736 MWHGEEGMAKALVASRL-----YVSLAKTASLATGIGMSQDTEFSDESSELAVELE 790
 QY 586 ECVNSBARAFALLVRNRCMSKTTCHLATEADAKAFPAHDGVAQFLTRIIMGDM---- 641
 Db 791 YCTHGGRDQTLRLITCGLANWGETCISLAANNCHRFLLHPPCCQMLSLDMOGGLMKN 850
 QY 642 -----AAGPILRLGAFICFALVYTNLITFSEBAPL-----TGLEDLQ 681
 Db 851 NQNSKVLTCIAAPPLIFLIGFTKEQMLPKTAABHDEBMSBEMKASBDTDTSSSS 910
 QY 682 DLDSLDE-----KSPVLGLQSRVELEAP---- 707
 Db 911 DSDSDDEDAKLRAOSLSADQPLSIHRLVRDKUNFSEKKKPDWG---ISRIVAAPPIVT 966
 QY 708 ---RAQ----- 710
 Db 967 GRNBARMSIKSKKNVIRKPACIKIETSDDEQOKKATEMCKSTFPDFPFPYINRT 1026
 QY 711 GDRGPRAV-----FLTR-----WRK---F 727
 Db 1027 GKGSVAVANNDMTYIDPSEELDTQRRKSRSESSRNVTVQVYQRLSMKKIMEF 1086
 QY 728 WCAPVTVFLGNVVMYFA---FLFTYVLLVDRPPPGSGREVTLTFWVFTLVLE-- 781
 Db 1087 YKAPITTYW---LWFFAIFWILLTYNLVKTQ---RIASWSWYVFAIYFVTTLEIGR 1140
 QY 782 EIRGFFTEDDTHLVKKFTLVYGDNNKCDMAIFLFTVGTCTMLPSAFEAAGTVALMD 841
 Db 1141 KVVSTIMMDSKVYLKQARVFFQYRNGLAFLGLTYLVIAFIRLSFTTTLGHLITICN 1200
 QY 842 FWFFTLRILHFAIKQCPKIIIVERMMKDVFFFLFSLVWLVAYGTTQALLPHRGR 901
 Db 1201 SVIWSLKLTVYLSVQOGLGPIYINIVAMIPMTPLVCVLVPTITLYAFGLMQSIYVYE-- 1258
 QY 902 LEW---IFRVLVLRPYLQIFGOIPLDEIDEARVNCSTHPLLEDSPCPSLYAN----- 952
 Db 1259 -DWHMILVRNIFLOPYFMYLGEVYAAEID-----TCGDEIWIQTHEBENIPISMLNVTHETC 1313

Db 970 QYANSPSCPS--OSLPAYLIVIEFVILKLLWPLIFAFPSKTAKNVDEADKIRFQLYS 1027

QY 1000 LIVEYHERPALAPPFL 1016

Db 1028 LAEDFLRPPPLPPLTI 1044

RESULT 7

JH0588

calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Mar-2002

C:Accession: JH0588

R:Phillips, A.M.; Bull, A.; Kelly, L.E.

Neuron 8, 631-642, 1992

A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with

A:Reference number: JH0588; MUID:92232293; PMID:1314616

A:Accession: JH0588

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1124 <PRT>

A:Cross-references: GB:M88185; NID:9469057; PID:q158715

A:Experimental source: head

C:Genetics:

A:Gene: trpl

A:Cross-references: FlyBase:FBgn0005614

C:Superfamily: TRPC3 protein

C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein

F:341-363/Domain: transmembrane #status predicted <TM1>

F:374-396/Domain: transmembrane #status predicted <TM2>

F:462-479/Domain: transmembrane #status predicted <TM3>

F:512-533/Domain: transmembrane #status predicted <TM4>

F:549-572/Domain: transmembrane #status predicted <TM5>

F:643-668/Domain: transmembrane #status predicted <TM6>

F:710-727/809-825/Region: calmodulin binding #status predicted

F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 4.3%; Score 262.5; DB 2; Length 1124;

Matches 181; Conservative 147; Mismatches 269; Indels 349; Gaps 43;

QY 295 DIVRWTKLQNTITSHQHL-----LTVYDFEFGSSELDVTIL-----KALVK 336

Db 53 DHPNVRRIQKALRHQHNININCMDPLGRALTL-AIDNENLEWELVVMGVETDAILH 111

QY 337 ACKSHSQEPODYUDEKLAV-----ANDRVDIASSEIFNGDVEMKSCDLEAWDALV 389

Db 112 AINAEFEVAVELLEHEELIYKGEFYSQKVDI-NTAMFAPDI-----TPTMLAH 162

QY 390 SKKPEFVRLFVNGA--DVADFLTYGRLOELVRSVRSKSLFDLLQKQEARLTLAIG 447

Db 163 KNNFELRLILDRGAAPVPFPHDIRG-CEECVRLTDEBL-----RHSLSRYN 209

QY 448 TQOAREPP-----AGPPAFSLHEVSRLKD--FLDADCRGFYODGPDRRRAEKGP 499

Db 210 IYRALCSPFLICLSTNDPSSTAFOQLSWEIRNLALTQCECKSEYMD---LRQCCQFAVD 265

QY 500 RRTGQKWLDDNOKSINPRDLFLMAVLQNRHEMATYFMAQOEGVAAALAAKLKEMS 559

Db 266 -----LLDQRTSNE-----LAILLVYDPMSSY-----EPG----- 292

QY 560 HLETEAARATREAKYERLALDLFSECSNSEARAFALLVRRNRCMSKTCCLHLEAD 619

Db 293 -----DKMSL-----TRLVQALISK 307

QY 620 AKAFAHDGVOAFLTRIMWDMMAAGTPILR--LLGAFLCFALVYTNLTTFSEAPLRTG 676

Db 308 QKKFVHNSIQQLSSITWD---GLPGFRKRSIVDKVICIAQV---AVLF----- 351

QY 677 LEDLDLDSLDTEKSLYGL-----QSRVEELVEAPRAQGRGPAVALLTRMRKFMGA 730

Db 352 -----FLYCLIIYWCAPNCRGTQGLM-----RK----- 372

QY 721 PVTYFLGNVWYFAFLPFLFVTVLV-----DERPPQSGSG 766

Db 373 PFMKFLIHASSYLFPLFI---LIVSQRADDDFVARIFGTMYKKELACQELRQROQTBSK 429

QY 767 PEVTLVFWVFTLVLEIRQGFTEDETHLVKKFTLYVDNNKNCMVAFLEFIVGTCRM 826

Db 430 LELIVMVYVIGFVWEEOVEIFAVGMS-----YLRNMNFIIDFLNNSLY-VSWC-L 479

QY 827 LPSAFEAQRTVAMD-----FMVFT-LRLIHIFAIHKOL 859

Db 480 RAFATYQATTEIARDPQMAIYIPREKMHDPDQLAEGFLAANVFSALKVHPSINHL 539

QY 860 GPKIIVERMKDV--PFFLFELSYMLVAAGVT-----TQALLPHDGLFW-- 904

Db 540 GPLQSLGRVIDIYKFFFIYTLVLFAPACGLNQLWYFAALEKSKCYLP-GBEADWS 598

QY 905 -----IRRV--LYRP-----YLQIFQIIPUDEIDAVNCSHLLLEDSPSCSYAN 952

Db 599 HGDSCMKRRRFGNLFESSQSLFWASFQVVGDDDFELSGIKS-----YTR 642

QY 953 WLVIILVTVPLTVLNLAMNLIAFSTYFOVQGNATPMWFORYNLIVEYHERPA-LA 1011

Db 643 FVGLIMPFSYIVNYVTLNLILIAMNSYAMIDHSPTENKFARTKLMSTFEDSATLP 702

QY 1012 PPFILSHLSLTRRVFKKEHKKREHLERDLPPDLQKVYTWETVQENFLSKMKRRR 1071

Db 703 PPFNVLPVKKVI-RIFRKS-----KIDRQSKKREGEQF 739

QY 1072 DSEGVLEKTAHVDLFIKYLGLREQ-----EKRIKLESQIN 1110

Db 740 SEYDINIR-----SLVRYVAAMIRKKNPNVSEDDINEVSEIN 779

RESULT 8

Protein R06B10.4 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: F88391

R:anonymus, The C. elegans Sequencing Consortium.

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genseq.nsl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.e

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F88391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-899 <STO>

A:Cross-references: GB:chr_III; PIDN:AAB95033.1; PID:g2746879; GSPDB:GN00021; CESP:R06B1

A:Gene: R06B10.4

A:Map position: 3

Query Match

Best Local Similarity 3.9%; Score 239; DB 2; Length 899;

Matches 165; Conservative 125; Mismatches 313; Indels 252; Gaps 38;

QY 349 LDELKLAAMBRVDIAKEIFNGDVEMKSCD-----EEVMVALVSNKPEFRLVVD 401

Db 32 LREKQFLSCERGDISGVRLKLAGISTTFNINCPLGRNALILAIENENIEMTELLLD 91

QY 402 NGADVADFLTYGRLOELVRSVRSKSLFDLLQKQEARLTLAIGTQOAREPPAGPA 460

Db 92 NHIEGTDAIIVAGEE---NVEAVEIIVENLEKMDKFSERQGVITHSAPTPITPIV 148

QY 461 FSLHVSRLKDFLODACRGFYODGPDRRRAEKGPAPR-----TQCKWL 508

Db 149 LAAH-----KQNYE--CIKFLD-----KKGTVRPHRDVACSCPECVAAEEDSL 191

QY 509 DINQSENPRDRLMAVL-QNRHEMATYFMAQOEGVAAALAAKLKEMSHLETEA 567

Db 192 RLSRSRINAYRALTPSLICLSARDPIIYAFELSW-----LKRISFIENBERT 240

```

Qy 568 ARATREANYERLALDIFSECYSNSEAPAFALIVRNRCMSKTTG-----LHAT 616
Db 241 DYEELSQCKQKCEVHMLDQVRGSKLE--VVLNHTTNAMHDVTSANYGNPEKLARKLAI 298
Qy 617 EADAKAFPAHOGVOVAFIRIWMGDMAAGTPIRLILGAFLCFALVYTNLITPSEEAFLRTG 676
Db 299 QLSQKRFPAHNCQQLLDIMY---EGVESVR-----CTNFIY-KLIYF----- 338
Qy 677 LEDLDDLSLDTSEKSPLYGLQSRVEELVAPRAQDGRGPAVFLI---TRMKFPGAVT 733
Db 339 -----ILGMLSPFLSL-----VYLAHSSMGQFAKKRFI 369.
Qy 734 VFLGNVVMYFAFLFITY-----VLLVD-----FRPPGSGSGEPTLYFWFT 777
Db 370 KFLSHSGSYIFELLILIMASQRMVYIDNLRDIDVDRKETRGP--PTIECAIFLWVLG 427
Qy 778 LVLBEIRQ-----GFTDEDTHLYKFTLYVGDNNMKCMVAIFLFIYVGTGML----- 827
Db 428 LIWEIKQLMEGGLYN-----YCRNLMLNLDITNSLYLCTTALRVAVYQVE 475
Qy 828 PSAFAEAGR-----TVLAMPFM-----VF-TLRILHIFAIHQQLGP-KII 864
Db 476 QEALRANSVHIAHLPRDWDAMDPTLSECFPATANIFSSKLVIHTVSPHLGLPKIS 535
Qy 865 VVE-----RMKQDV--FFFLFELSYMLVAVGTTOALLPHDGLWEMIFERV- 909
Db 536 LGELSEKFWKKTKLRCRMVYDIKVFMYVALVLFAPACGL-----NQLWYAYAMR 585
Qy 910 -----LYRPY-----LQIFGQIPLDEIDBARVNGS-----THPILL 940
Db 586 QNECNLYQYQYNEKSLSYKYEHLKSCODKYSKCSISYHTAETLEFWALFGLVDLTHFRLK 645
Qy 941 EDSPSCPSLYANMLVILLVTLVFLVNLVNLMLLAMPSTYPOVQGNATMFKQRNL 1000
Db 646 ED-----HFLSEMTQKTFGSCCCSIIVLMLLIMMSNSYQYISDQADIEMKFARSRL 700
Qy 1001 IVEYHERPA-LAPFILL--SHLSLTLRVFKKEAKHREHLERDLPPDLQKVVWT 1056
Db 701 FLEYEDDTATLPPFPNIIVSPKSIYCYLHYLTKLKCNCTK-----LQQPSQKSM--R 751
Qy 1057 VQKENFLSKMKRRR 1071
Db 752 VESKMLAIRORPRKO 766

```

RESULT 9

S44873
ZC21.2 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44873
R:Du, Z.; Waterston, R.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans coemid ZC21.
A:Reference number: S44649
A:Accession: S44873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-823 <DUZ>
A:Cross-references: EMBL:L16685; NID:q289729; PIDN:AAA28168.1; PID:q289732
C:Genetics:
A:Insertions: 47/2; 91/3; 144/1; 215/2; 344/3; 394/3; 440/3; 506/2; 566/3; 756/3
C:Superfamily: TRPC3 protein
C:Keywords: transmembrane protein

Query Match 3.8%; Score 234.5; DB 2; Length 823;
Best Local Similarity 20.7%; Pred. No. 1.3e-08;
Matches 112; Conservative 92; Mismatches 195; Indels 143; Gaps 19;
Qy 549 LAACKILKEMSHLEFEAARAT---RAKYERLALDIFSECYSNSEAPAFALIVRRNR- 604
Db 260 LSAFKLSWDLQRLAFEEHEFKETYLQISEQCKQYSCDLLSQCRSSE--VIAIILKQGNV 317

```

Qy 605 -----CWS---KTTCLHATEADAKAFFAHDGVAQAFIRIWMGDMAAGTPIRLILGAF 655
Db 318 NDNINIDWASKLSTSLRLKLAIKYEQKAFVSHPHQQLTSTLWY-----EGIYRQSGTWA 373
Qy 656 CFALVYTNLITPSEEAFLRTGLEDLQDLSDLTSEKSPLYGL-----OSRVEELVAPRA 709
Db 374 NFFLYAFLLFLW-----PIFCIMYILMPKSRIGRLVRSP-- 407
Qy 710 QDGRPAVFLTLTRKRWGAPVTVFLGNVVMYFAFLFITYVLLVD-----R 758
Db 408 -----FMKFFYYSV-----FATFGLLTWATPEDRYRKGEGGTR 445
Qy 759 PPQSGSP--EVLTYFWVFTLVEEIRQGFTEDEDTHLYKFTLYVGDNNMKCMVAIF 816
Db 446 ASDRGPATWESLVFTWVIGMLMSEIKQLM-----BEGFKRYRQNMNMLDFLMIC 497
Qy 817 LFIYVGTGRLMPSAPE-----AGRTVLAMDPMVFTLRILHI 852
Db 498 LYLCITISIRL--SAVYIFTYREDPYRYTVRTYMTSEBMLVABALFAVGAVFSPARITYL 555
Qy 853 FAHKQIGPKIIVERMMKQVFFFLFPLSVLVAVGTTOALLPHDGRLEWIFRRVLYR 912
Db 556 FQTPVYLGPIQISIGCMLVDKACFLFVLIISSFSIGLAQLYWYDPNTDCLPGATCK 615
Qy 913 PYLQIFGQIPLDEIDBARVNGSTHPLL-----EDSPSCPS-LYANMLVILLVTF 962
Db 616 HSNVPSFI-----ADSYLTLLMSLFSITKEDBDIVENHKITQVCGGMFTMY 664
Qy 963 LVTNVLMLMLIMFSYTFVOVQGNATMFKQRNL-IVEYHERPALAPF-TLSHL 1020
Db 665 HCTSIIVLMLMLIMMSHSPQIINDHADLEWKFRHTLMMAHFEGSSLPFPFNIIYTPK 724
Qy 1021 SL 1022
Db 725 SL 726

```

RESULT 10

trp3 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C:Accession: J05807
R:Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.
Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A:Title: Expression and characterization of a trp1 homolog from rat.
A:Reference number: J05807; MUID:98042538; PMID:9367904
A:Accession: J05807
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-828 <PRB>
A:Experimental source: brain
C:Comment: This protein participates in store-operated Ca2+ entry into cells.
C:Superfamily: TRPC3 protein

Query Match 3.1%; Score 186; DB 2; Length 828;
Best Local Similarity 19.7%; Pred. No. 4.4e-05;
Matches 153; Conservative 122; Mismatches 291; Indels 210; Gaps 31;
Qy 381 EEWVVDLAVNKPFFVRLFYDN-----GADVADFLTYGRLQELVRSVRKSL-LFDLQRK 435
Db 40 EERLDAAEYGNIFVVKMLBESITLWNCVDYVGNALQ---LAVGNHLEVEILLKK 96
Qy 436 QEERLTLAGL-----GTQAREPPAGRPAPFSLHESRVLKDPLQDAGRGFYDGRGDR 490
Db 97 ENLARIIDALLAISKGVYRIVEALISHPALAQOTLSPLE--LRD--DDFYUD----- 146
Qy 491 RRAKGPAPKPT-----GQKW-----LLDINQSENMRDILFAVAVLQNRHMT-- 535
Db 147 ---EDGTRFSPDITPIILAAHCHRYEVVHLLLGKREPHDYVCRCADCAEKORLWTF 203
Qy 536 -----YFWANGQEGVAAALAAACKILKEMSHLEFEAARATREAKYERLA 580

```

Db      204 HSRSRINAYKGSPEVLSSESDPVLTLHELSENELAKLANIEKEKRNDRKLSMGCKDFV 263
Qy      561 LDLFSEECYSNSBARA-----FALLVRNRNCWCKTTCLHLATADAKAFPAHDGVAFLTR 635
Db      264 VGVLLDLCRDSSEVEEVLINLNDLSEVEERHGHKASLRVKLAIKYEYKFAVPCQOQLLT- 322
Qy      636 IWMGMMAAGTPIRLRLGAFLCFALVYTNLITFSEEARPLTGLEDLODLSLTERKSPLYG 695
Db      323 IWMGMVSGREIAIKCL-VLVVALLALPFLAIGWTAPC----- 359
Qy      636 IQSRVEELVEAPRAQDGRPAVFLITRMKFGCAPVTVFLGNVVM-----YEPFLFLFTY 751
Db      360 --SRIGKILRSP-----FMKFAVASFIIFLLGLVFNADREGITLLPN 401
Qy      752 VLLVD-----FRPPQSGSGPEVTLVFWVFTLVLEIRGSGFTDEDTHLYKFKTLVGDN 806
Db      402 ITVIDYPRKQIFRVKTTQFTWTEMLIMVWVLGMMWSECKELMLEGPREYIVOL----- 453
Qy      807 WKKCMVAIFLFIYGVTCGML----- 827
Db      454 WVVLLFLSI--FLAFTARFLAFLQATKAQOYVDHVSDESLEVTLPREVQYFTARDKM 511
Qy      828 ----PSAFEGRTVLAMDPMVFTLRILHIFALHKQIGPKIIVERMMKQVF--FLLFELSV 882
Db      512 LPSDDQIISGLYALAV--VLSFSRIAYILPANESGFLQISLGRVNDQIFKFWLFIWV 569
Qy      883 WL-----VAVGVTQALLHPHGRLEWIFRRVLYRPLQIFGQIPLDEIDBARVNCST 935
Db      570 FLAFMIGMFLYSYLGAKVDPAFITVEESFKTLFW--SIFG--LSEV-----T 614
Qy      936 HLLLEDSPSCPS-----LYANMVLVLLVTPFLVTLVLMNLLIAMFSTFOVQGNATM 991
Db      615 SVVLKYDHAKFTENIGVLYGIYNTWV-----VLLNMILIAINSSYQEIEDSDV 665
Qy      992 FMKFORNVLIVEYHERPALAPPEIL--LSHLSTLRRV-FKKEAEKREHLERDL 1043
Db      666 EKKFARSKMLSLFSDGCKTLPPPLVPCPSFVYFIRIRYNPR--CRRRLRQKDI 718

```

RESULT 11

```

S68238
trp-1 proteain - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S68238
R:Zhu, X.; Chu, P.B.; Peyton, M.; Birnbaumer, L.
FEBS Lett. 373, 193-198, 1995
A:Title: Molecular cloning of a widely expressed human homologue for the Drosophila trp
A:Reference number: S68238; MUID:96033971; PMID:7589464
A:Accession: S68238
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-793 <ZHU>
A:Cross-references: EMBL:U11110; NID:g1072042; PIDN:AAA93251.1; PID:g1072044
C:Superfamily: TRPC3 protein
C:Keywords: alternative splicing

```

```

Query Match      2.8%; Score 170.5; DB 2; Length 793;
Best Local Similarity 18.0%; Pred. No. 0.00055;
Matches 115; Conservative 106; Mismatches 216; Indels 203; Gaps 27;

Qy      555 LKEMSHLETE-----AARATREAKYERLALDLFSEECYSNSBARAF----- 596
Db      244 LKELSLVEVEFRNDYBELAR-----QCKFAKDILAQARNSRELEVIINHTSSDEPLDKR 298
Qy      597 ALLVRNRNCWCKTTCLHLATEADAKAFPAHDGVAFLTRIMWGDMAA--GTPIRLLGAF 654
Db      299 GLLEER---MNLRLKLAIKYKQKEFVSQNCQOFLNTWPGQMSGYRRKPTCKKIMTV 354
Qy      655 LCFALVYTNLITFSEEARPLRTGLELDLODLSLTERKSPLYGLQSRVEELVEAPRAQDGRG 714
Db      355 LTVGIFW-----PVLSLCYLI-----APKSO----- 375

```

```

Qy      715 PRAVFLTRMKFWGAPVTVFLGNVVMFAFLFTYVLLVDFRPPQSGSPG-----EV 769
Db      376 -----PRRIHTPRMKRIIHGASFTLLLNLSLV-YNEDKKNMTGMPALERIDY 425
Qy      770 TLFWVFTLVLEIRGSGFTD-EDTHLYKFKTLVGDNMNKCDAVAFLLVGVTCGMLP 828
Db      426 LLIMTIOMISDIKRLWYEGLED-----FLEESRNQLSFVMSNLYLATFALKYVA 476
Qy      829 -----SAFEGRTVLAMDPMVFT-----RLHIFPAIHQIGPKIIVERMM 870
Db      477 HNKHFDEADRDMDAFHP--TLVABGLFAFANVLSTYLFPMYTTSSILGFLQISMGWL 534
Qy      871 KDV--FFFLFELSVLVAAGVTTQALLHPHGRLEWIFRRVLYRPLQIF--GQIPLDEI 926
Db      535 QDFGKFLGMFLVLVFSFTIGLT-----QLYKGYTSKQK 569
Qy      927 D-----BARVNCSTHPLLLEDSPSCPELYANMVL----- 956
Db      570 DCVGIFCQSGNDTFHSFI-----GTCFALF--WYIFSLAHVAIFVTRFSYGEELQSFVGA 623
Qy      957 LLVYFTLVTLVLMNLLIAMFSTFOVQGNATMFMKFORNVLIVEY-HERPALAPPE- 1014
Db      624 VIVGTYNVVAVIYVTKLVAMLHKSFOLIANHEDEKWFARAKLWLSYFDKCTLPPPN 683
Qy      1015 -----ILLSHLSTLRRVFKKEAEKREHLE--RDLPPDLQKVVTWETVQK----- 1059
Db      684 IIPSKTICWMLSSLSKIKCSHTSGKVKRQNSLKEMNMLQKRD-----ENVYKMWCC 737
Qy      1060 --ENFLSKMEKRRRDSGEVLRKTAHRVDYIAKYGLRE 1097
Db      728 LVHRYLTSMRQMGSTDOATVENINELRQDSKFENEIRD 777

```

RESULT 12

```

138361
TRPC1 proteain - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
C:Accession: 138361
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Steetten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: 138361; MUID:96003837; PMID:7568191
A:Accession: 138361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

```

```

Query Match      2.8%; Score 170.5; DB 2; Length 810;
Best Local Similarity 18.0%; Pred. No. 0.00056;
Matches 115; Conservative 106; Mismatches 216; Indels 203; Gaps 27;

Qy      555 LKEMSHLETE-----AARATREAKYERLALDLFSEECYSNSBARAF----- 596
Db      261 LKELSLVEVEFRNDYBELAR-----QCKFAKDILAQARNSRELEVIINHTSSDEPLDKR 315
Qy      597 ALLVRNRNCWCKTTCLHLATEADAKAFPAHDGVAFLTRIMWGDMAA--GTPIRLLGAF 654
Db      316 GLLEER---MNLRLKLAIKYKQKEFVSQNCQOFLNTWPGQMSGYRRKPTCKKIMTV 371
Qy      655 LCFALVYTNLITFSEEARPLRTGLELDLODLSLTERKSPLYGLQSRVEELVEAPRAQDGRG 714
Db      372 LTVGIFW-----PVLSLCYLI-----APKSO----- 392
Qy      715 PRAVFLTRMKFWGAPVTVFLGNVVMFAFLFTYVLLVDFRPPQSGSPG-----EV 769
Db      393 -----FGRIHTPRMKRIIHGASFTLLLNLSLV-YNEDKKNMTGMPALERIDY 442
Qy      770 TLFWVFTLVLEIRGSGFTD-EDTHLYKFKTLVYGDNMNKCDAVAFLLVGVTCGMLP 828

```

```

Db      443 LLIIMTIGMINDIKRMWEGLED-----FLEESRNOISFVNSIYATFALKVYA 493
Qy      839 -----SAFEAGRTVLAMDPMVT-----LRLIHIFAIHKOLGPKIIVERMM 870
Db      494 HNKHFHDPADRKMDAFHP--TLVAEGLFAFANVLSTLRFMYTSSILGPIQISMGOVL 551
Qy      871 KDV--FFPLFELSWLVAVGVTTOALLPHDGRLEWIFRRVLYRPLYQIF--GQIPLDEI 926
Db      552 QDFKFLGWFLLVLFSPFTIGLT-----QLYDKGYTSKEQK 586
Qy      927 D-----EARNVCSGTHPILLEDSPSCPSLYANMVI-----956
Db      587 DVGVFCEBQSDNTHSF-----GTCFALF--WYFSLAHVAIPVRESYGELOSPVGA 640
Qy      957 LLLVTFLLVNLVNLMLIAMFSYTFQVQGNATVWFKFORNLIYEV--HERPALAPP- 1014
Db      641 VIVGYNNVWVIVLTKLVAMLMHKSFOLIANHEDEKWKAKAKMLSYDDKCTLPPEPN 700
Qy      1015 -----ILSHSLTLRRVFKKEAEHKEHLE--RDLPLDOKVVTWETVOK--- 1059
Db      701 IIPSEKTCYMTSSLSKWCSTHSGKVKVRQNSLKEMRWLKQKRD-----ENYQKVMCC 754
Qy      1060 --ENFLSKMEKRRRDESEVLAKTHRVDFIAKYIGIRE 1097
Db      755 LVHRYLTSMRQKOSTDQATVENLNELRDLSKFRNEIRD 794

```

RESULT 13

```

T34472.
hypothetical protein W03B1.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T34472
R.Miller, N.; Bradshaw, H.; Wu, X.; Gattung, S.
submitted to the EMBL Data Library, June 1998
A.Description: The sequence of C. elegans cosmid W03B1.
A.Reference number: Z21532
A.Accession: T34472
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-823 <MTL>
A.Cross-references: EMBL:U58753; PINN:AAC24437.1; GSPDB:GN00022; CESP:W03B1.2
A.Experimental source: strain Bristol NZ; clone W03B1
C.Genetics:
A.Gene: CESP:W03B1.2
A.Map position: 4
A.Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2

```

Query Match 2.7%; Score 166; DB 2; Length 823;

Best Local Similarity 22.4%; Pred. No. 0.0012;

```

Matches 99; Conservative 64; Mismatches 172; Indels 106; Gaps 19;
Qy      771 LYFWFTLV-----LEIRQ--GPTDETHLVKKFTLYGDNKKCDMAIFLFIYGV 822
Db      406 LAFWRIVLVPLLTLEAARLLIFAVIEKKSSDKNF-----WGLPI 452
Qy      823 TCRMLPSAFEGRTVLAMDPMVTFLRLIIFAIHKOLGPKIIVBRMKDV--FFPLPFLS 881
Db      453 TLELLYKALFAIAT-----VSTLARFHSIT--OSLGFTHLFKKMKVCMFLIFCT 502
Qy      882 VWLVAVGVTTOALLPHDGRLE--EWIFRRVLYRPLYQIFGQIPLDEIDARV---N 932
Db      503 FWFVL-----AVIHVSISRTLATSNSFLYVTFQKREIGEVQ---DEDRIGILLN 552
Qy      933 CSTHLLLED-----SPSCPSLYANMVIILLVTLFLLVNLVNLMLIAMFSYTFQV 985
Db      553 CSEYKRWAEFFDMEVAEASC--LFRSTIMPVVFYIFVGIILLVNLTLQLTREYNE 610
Qy      986 QGNATFMWFORNLIYEVHERPALAPPFL-----1017
Db      611 SKNSAYVYGYLKYEDUTKESLALPPPSLTYVVLRFVYSCFFKYIYITTWLTSGCCK 670
Qy      1018 --SHLSLTLRRVFKKEAEHKEHLELDLPDLQKVVTWETVOKENFLSKME-----K 1068

```

```

Db      671 CSTAISLSLWNRNIVRIYEGPWGAVRQTDNEIDTKVAEFLRKKPDMALETKLDLVNNYD 730
Qy      1069 RRPDEGEVLKTHRV--DPIAKYLGRLREGEKIKCESQINCSYVSSVADVLQAQG 1127
Db      731 KDVDDE--EALKKLGKEIKKFLAKEIG--EERERQSNLENHPRSGSVLDPKKGRLS--- 784
Qy      1128 GPRSGHCEGSGOLVAADHRC 1148
Db      785 --RTFAPVPVGSASVSLDQEG 803

```

RESULT 14

```

528916
dystrophin - mouse
N.Alternate names: duchenne muscular dystrophy protein
C.Species: Mus musculus (house mouse)
C.Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C.Accession: S28916; B27162; S10922; C43837; B40134
R.Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.
Nucleic Acids Res. 20, 1725-1731, 1992
A.Title: Human and murine dystrophin mRNA transcripts are differentially expressed during
A.Reference number: S28916; MUID:92253376; PMID:1579466
A.Accession: S28916
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: mRNA
A.Residues: 1-3678 <BIE>
A.Cross-references: EMBL:M68859
A.Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
R.Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.
Cell 50, 509-517, 1987
A.Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary
A.Reference number: A90897; MUID:87273512; PMID:360877
A.Accession: B27162
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-201 <KOE>
R.Nudel, U.; Zuk, D.; Einat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe, D.
Nature 337, 76-78, 1989
A.Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain.
A.Reference number: S06461; MUID:85082658; PMID:2909892
A.Accession: S10922
A.Status: translation not shown
A.Molecule type: mRNA
A.Residues: 1-106 <NID>
A.Cross-references: EMBL:X14183
R.Rapaport, D.; Lederlein, D.; den Dunnen, J.T.; Grootscholten, P.M.; Van Ommen, G.J.; F
Differentiation 49, 187-193, 1992
A.Title: Characterization and cell type distribution of a novel, major transcript of the
A.Reference number: A43837; MUID:92316332; PMID:1377655
A.Accession: C43837
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 'MREHLKG', 3069-3181 <RAP>
A.Note: sequence extracted from NCI backbone
R.Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.
Science 238, 347-350, 1987
A.Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.
A.Reference number: A40134; MUID:88018015; PMID:3659917
A.Accession: B40134
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 300-676 'F', 678-1390 <HOF>
A.Cross-references: GB:M18025
C.Genetics:
A.Introns: 11/1
A.Note: The list of introns may be incomplete
C.Species: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystropi
C.Keywords: actin binding; alternative splicing
P.14-233/Domain: alpha-actinin actin-binding domain homology <ACT>
P.340-449/Domain: spectrin/dystrophin repeat domain homology <SP1>
P.450-558/Domain: spectrin/dystrophin repeat homology <SP2>
P.2797-2924/Domain: spectrin/dystrophin repeat homology <SP3>

```


F;3048-3085/Domain: WW repeat homology <WW1>

	Query March 158; Conservative	2.7%; Score 164.5; DB 2; Length 3678; Best Local Similarity 19.9%; Pred. No. 0.015; Matches 158; Conservative 99; Mismatches 266; Indels 269; Gaps 36;
Qy	60 WHLPAFLVSLVSGEOPFAMKSWLRDY-----LRKGLVKAAGSTGAWILTSALRVG	111
Db	2228 WLEBADNIAIRPLDGEQ--OLKEOLEGVKLAELPLFQIGLIKOLINTEGAVLVSA----	2281
Qy	112 LARVAGAVRHSLSASTSKYRVAVAGMASLGRVLHRIILEAEQEDPVNHPEDDGSQG	171
Db	2282 -----PIREEDDKLEKKLK-----OTNQMIKVSALPEKGELEVLHKD-----	2322
Qy	172 PLCSLDSNLSHFIL-VEBPFGKDGDLTELRLRKHSISEQAGYGTGSJIEI-----	223
Db	2323 -FRQLEQDLHLILWSP-----INQLEIYNQPSQAGPDIKEIEVTVHGKA	2370
Qy	224 PVLCLLVNGD-----PNTLERISRAVE-----QAAPFLILVGS	256
Db	2371 DVERILSKGQHLVYKEKPEST-QPVRRKLEDLRSEWAVNHLRELRTKQDRAPGLSTTGA	2429
Qy	257 GGIADVLALVNQPHLLVPVKAEEKFKEFPSK-----HFWEDIVRWTKLLQN	305
Db	2430 S--ASQYTLVLTQSGVTKEVYSKL--EMSSSLLLEVPALADNRAMATELTDWLSLDR	2484
Qy	306 ITSQHLI-----TVYDFEGESSELDTVILKALVKACKSHSGSEPODYL	349
Db	2485 VIKSORVAVWGLEDINEMIIKOKATLODLBOR-PROLELITTAONLNKNTSNOEAR11	2543
Qy	350 DEL--KLAVADRVD-----IAKSEIFNDVEMKSC--DLEFYM-----	384
Db	2544 TDRIERITQWDEVOEOLQNRQOLNEMLKSTQWLKAKEAEBOYIGVRGKLSMKEGP	2603
Qy	385 --VDALVSNKBEFVRLFVD--NGADVADFLTYGRLOELRYSVRSKSLFDLLORKE	437
Db	2604 HTVDAIQRKITEKQALDKLRQRLSVADVANDLKLRLDYSADPTRK-----VHMIT	2657
Qy	438 EARLITLGLGTOQAREPPAPAFSLHESVNLDF-----LQDA	477
Db	2658 NINTSWGNIHRVSEQENA--LEETHLLLOOFULDERKFLSWITEAETNAVNLQDA	2711
Qy	478 CR--GFYODGRPGDRRAE-----KGPAREPT-----GOKWLDLNOKSENPMWL	521
Db	2712 SRKEKLELDSR-GVRELMKPMQDLOGELEIETHTDIYHNLDENQKILRSLESDAP----	2766
Qy	522 FLMAVLQNRHEMATYFWAMGQGVAAALACKILKEMSHLETEAARATREAKYERIAL	581
Db	2767 ----LQORRLNNMFKWSLEQ-----KSLNIRSHLEASSD-----QMKRLHT	2805
Qy	582 DLFSBCYSNSEARAFALVRRNRCSKTTCLHLTEAARAKAFPAHDVGQAFLETRIMWQDM	641
Db	2806 SLQE-----LLV-----WLQKDELSQAQIIGDFPAVQKQNDIHRAPKREL	2848
Qy	642 AAGPTIIRLLGAFLCFALVYTNLITFSEEARLRTGLELDQDLSDITEKSPLYGQSRVE	701
Db	2849 KTKPEPVI-----MSTLETVRIFLTEQ-PLGEKELKYQ	2879
Qy	702 ELVEAP---RAQ 710	
Db	2880 EPRELPEERAQ 2891	

A;Reference number: S61643

A;Accession: S61648

A;Molecule type: DNA

A;Molecule type: DNA
A;Residues: 1-482 <H1

A;Residues: 1-482 <BEN>
A;Cross-references: EMBL:X94335; NID:q1262139; PID:q1164934

A; Cross-references: EMBL:X94335; NID:g1262139; P1D:g1164934
R:Voas, H.; Benes, V.; Rechmann, S.; Tedorch, C.; Schwager, C.; Paces, V.; Ansdorfe, W

R; Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schmitt, H. Submitted to the Protein Sequence Database. July 1996.

submitted to the Protein Science Database. Accession number: 66606E.

A;Reference number:

A;Accession: S66973

A;Molecule type: DNA

A;Residues: 1-482 <VOS>
A;Molecule type: DNA

A;Residues: 1-482 <VOS>
A;Cross-references: EMBL:Z74995; NIT

A; Cross-references:
A; Experimental source

A; Experimental source: strain S4

C;Genetics:

A;Cross-references: SGD:S0005614

A:Map position: 15R

C/Superfamily: *Saccharomyces cerevisiae* probable memb

C/Keywords: transmembrane protein

F:46-62/Domain: transmembrane #status predicted <TM1>
C;keywords: transmembrane protein

F:159-175/Domain: transmembrane #status predicted <TMI>
F:46-62/Domain: transmembrane #status predicted <TMI>

Accession	Protein	Length	Weight	PI	Transmembrane	status	predicted	TM
F159-175/Domain	transmembrane	17	2000	4.5	1	status	predicted	TM
F184-200/Domain	transmembrane	17	2000	4.5	1	status	predicted	TM

Query Match 2.5%; Score 153.5; DB 2; Length 482;

Query Match	2.5%	Score 153.5; DB
Best Local Similarity	20.1%	Pred. No. 0.0044

Best Local Similarity 20.1%; Pred. No. 0.0044;
Matches 95: Conservative 79: Mismatches 151: Indels 147: Gaps 19

```

QY 702 ELVAPRAQGR-----GPRAVFLTRKREKGAUVTLGVMVYFAFLFLFTVYL 753
Db 4 ERMSPPKLSGSHNPFYQGRFTGGSVIDLSFQRRKIGACIPKLPADLL-----ILFGLGYTL 60
QY 754 LVDRPPEQSGSGBEVTLVFWFT--LVLEIRQCFP-----DEPTHLYKKT 800
Db 61 VYNGKDSERVSFDLESIFVVFNTGTFLDETLYKYUYGYAHLSEFWNLFNDTYLITFA 120
QY 801 L-----YVGNMNRKCDKVAIFLFIVGTCTMLBSA--FEAGRYTLAMD FWF 845
Db 121 MGFRA MSTPLPNAKXSSEMDX-----ISRYVLSCAAFVMSRLLYESQRF 168
QY 846 TLRLLHFAHKOQCPKIYVERRMKD--VFFFLFPLSVLVYAVYVTTQAL--LHNDGL 902
Db 169 -----IGIMLVILKMKKESIVFFFLF-----LIMGFTGGLSDSADGR 211
QY 903 EMIFRRVLYRBYLOIFQOIPLEIDEAIVNCSNTHLEDSBSCPSTLAMYLVILLYLF 962
Db 212 D-IGPLIGNLITVYLGSGFDVEE-----FAPRYAIIUYGY 249
QY 963 LLVTVVILMNLIIAMFSTYFOVVOGN-----ATYFMKFOR-----NLT-- 100
Db 250 YFIVSVILENLIIALYSTAYQKVDINADEXMALMSQTLRIRAPDEDEVVSPNLLEV 309
QY 1002 -----VEYHERPALAPFILLSLTLRRVFKKAEAKHREHLERDLP 1041
Db 310 FMTPIFRILPRKAKDLSYTWVTIYSPFLIISYKET-----REARRIKYRMKRLAND 363
QY 1046 PLDDQKVTVWEYQ-----KENFLSKWEKR--RDSSEGVLAKTARVD 1086
Db 364 DANEDVTWDLTLDGYLDDDGFLFSNNRNSGMPATOLKNSRSILKORTLAEQED 415

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using SW model

Run on: September 10, 2003, 09:27:29 ; Search time 17 Seconds

(without alignments)
3222.712 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6091
Sequence: 1 MODVGGPPRSGDAEDRRE.....HRGGIDGWEQDAGQPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041	33.5	1503	1	TRP2_HUMAN
2	655	10.8	1017	1	TRP3_HUMAN
3	318	5.2	1275	1	TRP_DROME
4	290	4.8	1418	1	CEIL1_CAEEL
5	262.5	4.3	1124	1	TRP1_DROME
6	258.5	4.2	1172	1	TRP2_MOUSE
7	244	4.0	885	1	TRP2_RAT
8	239	3.9	1027	1	TRP1_CAEEL
9	231	3.8	973	1	TRP5_HUMAN
10	231	3.8	974	1	TRP5_RABIT
11	231	3.8	975	1	TRP5_MOUSE
12	221	3.6	981	1	TRP4_BOVIN
13	219.5	3.6	977	1	TRP4_HUMAN
14	216	3.5	974	1	TRP4_MOUSE
15	216	3.5	977	1	TRP4_RAT
16	194	3.2	931	1	TRP6_HUMAN
17	193	3.2	862	1	TRP7_HUMAN
18	190.5	3.1	836	1	TRP3_MOUSE
19	187	3.1	862	1	TRP7_MOUSE
20	183	3.0	840	1	TRP6_MOUSE
21	180.5	3.0	938	1	TRP3_HUMAN
22	179.5	2.9	736	1	TRP3_RAT
23	178.5	2.9	759	1	TRP1_RABIT
24	171	2.8	793	1	TRP1_BOVIN
25	170.5	2.8	759	1	TRP1_RAT
26	170.5	2.8	793	1	TRP1_HUMAN
27	170.5	2.8	809	1	TRP1_MOUSE
28	164.5	2.7	3678	1	DMD_MOUSE
29	152	2.5	432	1	TRP2_BOVIN
30	150	2.5	968	1	PKD2_HUMAN
31	148.5	2.4	966	1	PKD2_MOUSE
32	140	2.3	3680	1	DMD_CANFA
33	136	2.2	5596	1	MDNL_HUMAN

34	132	2.2	830	1	VPP3_HUMAN	Q13488 h vacuolar
35	130.5	2.1	2390	1	SECP_HUMAN	O15020 homo sapien
36	129.5	2.1	1261	1	ADAF_BRARE	O919h8 brachydanio
37	128.5	2.1	3685	1	DMD_HUMAN	P11532 homo sapien
38	128	2.1	621	1	P212_MOUSE	O911g4 mus muscicu
39	126.5	2.1	2388	1	SECP_RAT	O9qwm8 ratu
40	124.5	2.0	1835	1	CCAI_RAT	O920y8 ratu
41	124.5	2.0	5065	1	EBPL_HUMAN	P58107 homo sapien
42	123.5	2.0	2223	1	CCAI_HUMAN	O9pox4 homo sapien
43	123	2.0	1060	1	AZII_MOUSE	O62036 mus muscicu
44	120	2.0	2019	1	CIN5_RAT	P15389 ratu
45	119	2.0	1087	1	XPO7_HUMAN	O9uia9 homo sapien

ALIGNMENTS

RESULT 1
TRP2_HUMAN
ID AC 094759; 096XN6; STANDARD; PRT; 1503 AA.
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Long transient receptor potential channel 2 (LTPC2) (Transient
DE receptor potential channel 7) (TRPC7).
GN TRP2 OR LTPC2 OR TRPC7 OR KMP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain.
RX MEDLINE=99026133; PubMed=9806837;
RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Ito F.,
RA Shimizu N.;
RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)
RT highly expressed in brain.";
RL Genomics 54:124-131(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX Wehage E., Eisfeld J., Heiner I., Juenling E., Zilt C.,
RA Lueckhoff A.;
RT "Splice variants of LTPC2 differentially activated by ADP-ribose an
RT hydrogen peroxide.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Torok Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Tauden S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhaber M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Saeki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P.,
RA Scharte M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieseemann L., Dagand E.,
RA Wehmer J., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehnach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
CC -1- FUNCTION: MAY BE A CALCIUM CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=094759-1; Sequence=Displayed;
CC Name=2;
CC IsoId=094759-2; Sequence=VSP_006574, VSP_006575;
CC

```

CC -1- TISSUE SPECIFICITY: Highly expressed in brain.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB001535; BAA34700.1; -
CC EMBL; A417076; CAD01139.1; -
CC EMBL; AP001754; BAA95563.1; -
CC Genew; HGNC:12339; TRPM2.
CC
CC MIM; 603749; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005262; F: calcium channel activity; TAS.
CC GO; GO:0006816; F: calcium ion transport; TAS.
CC InterPro; IPR002111; Cat_channel_TrpL.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR002153; Trans_receptor.
CC Pfam; PF00520; Ion_trans.1.
CC Pfam; PF00293; NUDIX.1.
CC DR PRINTS; PRO1097; TRANSRECEPTR.
CC DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC Alternative splicing.
CC
CC FT DOMAIN 1 752
CC FT TRANSMEM 753 773 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 774 795 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 796 816 POTENTIAL.
CC FT DOMAIN 817 820 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 821 841 POTENTIAL.
CC FT DOMAIN 842 896 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 897 917 POTENTIAL.
CC FT DOMAIN 918 936 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 937 957 POTENTIAL.
CC FT DOMAIN 958 1025 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 1026 1046 POTENTIAL.
CC FT DOMAIN 1047 1503 CYTOPLASMIC (POTENTIAL).
CC FT VARSPLIC 538 557 Missing (in isoform 2).
CC FT VARSPLIC 1291 1325 DTLPELSTIQYVNVDDLDRSRSPHGYTVQAGLPL -> E
CC (in isoform 2).
CC FT FT /FTid=VSP 006575.
CC FT CONFLICT 1088 1088 S -> N (IN REF. 2).
CC FT CONFLICT 1189 1189 R -> Q (IN REF. 3).
CC FT SEQUENCE 1503 AA; 171225 MW; AD329AE79F1A71B5 CRC64;

```

```

Query Match 33.5%; Score 2041; DB 1; Length 1503;
Beet Local Similarity 38.8%; Pred. No. 4,4e-129;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGSGKRGKFRVPSGVAAPSVLFDLLLAEMHLPAPNLVSLVGEOPFAMKSWLR 85
DB 128 GILVFTGLSQKVKYKVRVSGODTPSSVIYHLMQHWLDVFNLLISTGAKFNKKPRXK 187
QY 86 DVLKRGVLVPAOSTGAWILTSALRVGLARHVGQAVRDSLASTSTKRVAVAGMSLGRV 145
DB 188 SIFRRRLVKAQTTGAMITGSGHGTVMKQVGEAVRDFSLSSYKGEGLITIGVATWGTV 247
QY 146 LHRRLIEEAQDEPPVHYPPEDDGSOGPLGSLDSNLSHFLIVGEPGKGDGLTELRLRE 205
DB 248 HRREGILHPTGSPAPYILDEDEG-OGNLTCCLDSNHSHPFLVDGTHGYVEIPLRTRLE 306
QY 206 KHISEGAGYGGTSGIIEIPVLCILVGDNPNTLERSRAVEQAPWLLIVSGSGIADVLAA 265
DB 307 KRISBGTKRGGV-AKIPICVAVLEGGCTLTHTINAATTNGPCPVVSGSRVADVINO 365
QY 266 LVNQP--HLVPRVAKQ--FKKFPSPKHSFMSMEDIVRTKLLQNTSHOHLITVYDFEQ 320
DB 366 VANLPVSDITISLLOOKLSVFQEMFET--FTESRIVETWTKKIODIVRRQLLTVFRBEGK 423

QY 321 EGSEELDTVILKALVAKCKSHSQEPQDYLD-ELKLAVAMRVDAIKSEIFNGDVEMKSCD 379
DB 424 DGQGVDAVAILLOALLKASRSODHFEHNMWDQKLAVAMNVDIARSSEIFNDEMOMKXSD 483
QY 380 LEEVNVDAIVSNKEPEFVLFDNGADVADFLTYGRLQELYSVSRSKSLFDLLQKQDEBA 439
DB 484 LHPITWALLISNKEPEFVLFDNGADVADFLTYGRLQELYSVSRSKSLFDLLQKQDEBA 538
QY 440 RLTLAIGLGTQARERPAAP--PAPSLHVSXVLDLQDADCRGFYQDQRRPQDGR 492
DB 539 -----VLVEDPERACAPAPRLQMHHVAOVLRELLDFTQPLVPRPHNDRLLLPV 592
QY 493 -----AEKGAPKPTGCKWLLDNOKSENPWRLFLMAVLONHEMATYFWAMQO 542
DB 593 PHVKLVNQGVSLSRSYKSSGHVTF-----TMDIRLLLTWALYQNRRELAIGTIWASQ 646
QY 543 EGVAALAAACKILKEMSHLETEAEAR--ATREAKYERLLDLFSECYSNSSEARAFALL 599
DB 647 DCIAAALACKILKELSKSEEDTDSSEMLALAE-EYEHRAIGVFTECYRKDEERAOKLL 705
QY 600 VARNKCSKTTCLHATENDAKAPFAHDGVAQAFILRIWGDMAAGTPILRLIGALFLCAL 659
DB 706 TRVSEAMGKTCTCLQALAKOMKFEVSHGIGAFILKVMWQSLVDNGLMRVTLCLMLAPPL 765
QY 660 VYTNLITPSEAPARTGLEDLQDDSLDTERKSPLYGLSRVELEYEARPAQDGRPAVVF 719
DB 766 LITGLISFREKR-----LQD-----VGTPLA----- 786
QY 720 LLTRNRKFWGAPVTVELGNVVMYFAFLFLFTYVLLVDRPPPGSGSEVTLFYFVFTLV 779
DB 787 ---RARAFPTAPVVVFHNLISYFAFLCLFVAVLMDPQV---PSWCECAIYLLMLFSLV 840
QY 780 LEEIQGFTEBDTHLYKKFTLYVGDMMNKKCDMAIEFLTYGTCRMLPSAFEGRTVLA 839
DB 841 CEEMQQLFYDDECGLMKKAALYFSDFMNKKLDVGAILLFGVGLTCRLIPATLYPERVLS 900
QY 840 MDMFWFTLLIHIFAIHQLGPKITIVERMMKDVFFFLFSLVWLVAAGVTTQALLHPHD 899
DB 901 LDFILFCRLKHIIFISTIKLGPKITIIVRKMKDVFFFFLAIVVWSGVAKQALLINE 960
QY 900 GLEWIFRRVLYRPLYQIFGOIP--LDEIDEARVNC--THPLLEDSPECPSP----- 948
DB 961 RRVDWLFGAVYHSLTIFGQIPGYIDGVNFEHSCBNGTDPY-----KPCPCESDATQO 1016
QY 949 --LVANMLVILLVFTLVTVNLLIMNLLIAMESYFOVVOGNATMFKFORNYLIVEHE 1006
DB 1017 RPAPEMELTVLLCLVYLLFTNLLNLIMFNVTFOQVQEHDTQIMKFORHDLIEEYHG 1076
QY 1007 RPAALPFFILSHLSLTLRVRFKKEAERKREHLERLDPDLDQKVVTMETVQKFNFLSKM 1066
DB 1077 RPAAPFFILSHLOLFKRVVLTVPRAKRHOLKRNKLEKNEALLMSIEIYIKENYVLONR 1136
QY 1067 EKRRRDSGEVLRKTAHRVDFIAKYL-----GLREQERKIKLESQINYSGLVVS 1118
DB 1137 QFOQKORBEQKIEDISNKVDAMVDLLDPLKRSQSM---RQLASLIEEQAQTRALHW 1193
QY 1119 VADVLAQGGGRSSQHGEGSOLVAAD--HRGIGDSHEQGG 1157
DB 1194 IVRTLRAQGSSEADVPITMSQKAAEBPDABPGGRKKTTEPG 1235

RESULT 2
ID TR13 HUMAN STANDARD; PRT; 1017 AA.
AC Q9HCF6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Long transient receptor potential channel 3 (LTRPC3) (Fragment).
GN TRPM3 OR LTRPC3 OR KIAA1616.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



```

DR EMBL; M18634; AAA28977.1; -.
DR FlyBase; Fggn0003861; trp.
DR GO; GO:0016028; C:habdome; IDA.
DR GO; GO:0008377; P:light-induced release of calcium, from inte. .; IDA.
DR GO; GO:0009416; P:response to light; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_trpl.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR002153; Trans receptor.
DR InterPro; IPR004729; Trp_Catchannel.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PRO1097; TRANSRECEPT.
DR SMART; TIGR00870; trp; 1.
DR TIGR; TIGR00870; trp; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 1.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW Vision; ANK repeat; Repeat.
FT DOMAIN 1 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 POTENTIAL.
FT TRANSMEM 388 390 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 391 411 POTENTIAL.
FT TRANSMEM 412 418 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 419 439 POTENTIAL.
FT TRANSMEM 440 450 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 451 471 POTENTIAL.
FT TRANSMEM 472 507 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 508 528 POTENTIAL.
FT TRANSMEM 529 541 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 542 562 POTENTIAL.
FT TRANSMEM 563 638 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 639 659 POTENTIAL.
FT TRANSMEM 660 1275 EXTRACELLULAR (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 143 172 ANK 2.
FT REPEAT 285 288 GORQ -> ASSE (IN REF. 2).
FT REPEAT 326 329 RRKO -> POE (IN REF. 2).
FT REPEAT 365 374 KPVKFTHS -> NPLSSSRTP (IN REF. 2).
FT REPEAT 785 785 S -> N (IN REF. 2).
FT CONFLICT 785 785
SQ SEQUENCE 1275 AA; 142589 MW; 91CFDD9896989B1 CRC64;

Query Match 5.2%; Score 318; DB 1; Length 1275;
Best Local Similarity 19.9%; Pred. No. 3e-13;
Matches 183; Conservative 133; Mismatches 276; Indels 328; Gaps 39;

QY 274 VPKVAEK-QPKKPKSHPSMEDIVRWYKLLQNTSH-----QHLLTYDFPEQEGS 323
DB 48 VKKILEYOGTDKF---NINCTDPMNRSAISAIENENFDLWVILLENHIEVDALLHAI 104
QY 324 EELDTYVILKALVAKCKSHSOPEDYDELKLAAMRVDAKSEIFNGDVEWKSCLLEV 383
DB 105 SEEYVAEVELLQWEEFNHKEGQPY-----SWEAVDSKS-TTVVDI-----TP 147
QY 384 MVDALVSNKEEFLFVDNGA-----DVADFLTYGRLO-ELYRSVSR 424
DB 148 LILAAHRNNVEIKILDRGATLPMRHVYKCGDECVTSOTTSLSHSGRIAYALSLA 207
QY 425 KSLFLDLQRKQSEARITLGLTQARPPAPPAFSLHEVSRLK--DFLODACKRGFY 482
DB 208 SSLI-----ALSSRD-----PVLTVQLSWEMLKRLQAMESSEFRAEY 243
QY 483 QDRPDRRAEKGPAKPTGCKMLDINKSENPMRDFLMAVLQNRHMAFYFAMQ 542
DB 244 TEMR---QWVDFGTS-----LIDHARTS-----MELEWMLFNHPSHDICLQ 286
QY 543 EGVAALAAACKIKEMSHLETEAARATREAKYERLALDLFSECVNSSEARAFALLVR 602
DB 287 -----RQTLER----- 292
QY 603 NRCWSKTTCLHLATEADAKAFPAHDGVAFLTRIWMGDMAAGPPIRLGLAFLCPALVYT 662
DB 293 -----LKLAIKYOKTFVAFHPNVQQLAAIWD-----GLPGFR----- 326

```

```

QY 663 NLITFEAPLRGTGLIEDQLDLSLDTKPSPLYGQSRVEELVEAPAGDGRPAVFLLT 722
DB 327 -----RKQASQQLMDVVKKG-CSPFYSL-----XYILAPDSEGG----- 359
QY 723 RWRKMGAPVTVFLGAVNMVPAFLFL-----FYVL--LVDRPFPQG 763
DB 360 --AKEMRKPVKFTIHSCTSYMFLLMLGMAASLRVQITFELLAPFMTLMDMEWKBERG 417
QY 764 --PSGEVTLVFWVTVLEER---QGFTDEDTLWKKFTLVGGMNKKCDVAFIL 817
DB 418 SLPCPIELAITTYMALIFEBKSLYSDGLE-----YIMDMIVDIYSNMF 465
QY 818 FIVGTCR-----MLPS--AFEGRTVLAMDENVF 845
DB 466 YVTWLICGATAMVIVHRDLWFRGIDPPRREHMHPFDPMLLSEGAFAAG-----WVF 517
QY 846 T-LRLIHFPAHKQGPRTIIVERMKGVFFFLFSLVLAAYGTTQALL----- 895
DB 518 SYLKLVIHFSINPHLGPLQVSLGRWIIDIIKFFFTYTLVLAFAFGGLNQLMVALEKN 577
QY 896 ---HHDRLEW-----IFRRV--LYRP---YLQIPQIDPDEIDEARVNCSTPL 938
DB 578 KCYHLHPDVADPDDGEKACTIWRRSNLFETSQSLFWASFGVLVDLVSFDLAGINS----- 632
QY 939 LLEDSPSCPSTLYANMLVILLVTFPLVTNVLMLMLIMFSTYEQVVOGNATMFWKFOR 998
DB 633 -----FTRWALMGSGSYVINIYVLNMLIMMNSYQIISERADTEKFAFS 681
QY 999 NLIVEYHE-RPALADPFLSHLSTLRRVFEKEAHEKHEHLERDL--PDPLQCVTW 1055
DB 682 QLMMSYFPGDGTIPPPFPCPMKMLRKTGKRPSRTKSPFKRSKMERAPQTLHDKVM--- 738
QY 1056 TVQKNEFLSKMKEXRRRDEG 1075
DB 739 KLVRRYIT-AEQRRDDYG 757

RESULT 4
CELL_CAEEL STANDARD; PRT; 1418 AA.
ID CELL_CAEEL
AC P34641;
DT 01-FEB-1994 (Rel. 28; Created)
DT 01-FEB-1994 (Rel. 28; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Ced-11 protein.
GN CED-11 OR ZK512.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodietinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lathille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy K., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its

```


RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Sprelling A.C., Stapleton M., Strong R., Sun E.,
RA Switek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
CC Science 287:2185-2195(2000).
CC -1- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.
CC SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M88185; AAA28979.1; -
CC EMBL: AE003832; AAM68793.1; -
CC PIR: JH0588; JH0588.
CC DR GO: GO:0016021; C: integral to membrane; NAS.
CC DR GO: GO:0016029; C: rhodomere; IDA.
CC DR GO: GO:0015075; F: ion transporter activity; NAS.
CC DR GO: GO:009628; P: response to abiotic stimulus; IMP.
CC DR InterPro: IPR002110; Cat channel_TrpL.
CC DR InterPro: IPR005821; Ion trans.
CC DR InterPro: IPR005820; M+channel_nlg.
CC DR InterPro: IPR002153; Trans_receptor.
CC DR InterPro: IPR004729; Trp_CatChannel.
CC DR Pfam: PF00023; ank; 2.
CC DR Pfam: PF00520; Ion_trans; 1.
CC DR PRINTS: PRO1097; TRNSRECEPT.
CC DR SMART: SM00248; ANK; 2.
CC DR TIGR: TIGR00870; trp.1.
CC DR PROSITE: PS00088; ANK_REPEAT; 1.
CC DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
CC DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC KW Calmodulin-binding; Vision; ANK repeat; Repeat.
CC FT DOMAIN 1 340 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 341 361 POTENTIAL.
CC FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 374 394 POTENTIAL.
CC FT DOMAIN 395 431 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 432 452 POTENTIAL.
CC FT DOMAIN 453 512 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 513 533 POTENTIAL.
CC FT DOMAIN 534 548 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 549 569 POTENTIAL.
CC FT DOMAIN 570 645 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 646 666 POTENTIAL.
CC FT DOMAIN 667 1124 CYTOPLASMIC (POTENTIAL).
CC FT REPEAT 78 107 ANK 1.
CC FT REPEAT 152 181 ANK 2.
CC FT DOMAIN 710 727 CALMODULIN-BINDING (POTENTIAL).
CC FT DOMAIN 809 825 CALMODULIN-BINDING (POTENTIAL).
CC FT CONFLICT 228 229 II -> SS (IN REF. 1).
CC FT SEQUENCE 1124 AA, 127749 MW, AF6323BA27626583 CXC64;
Query Match 4.3%; Score 262.5; DB 1; Length 1124;
Best Local Similarity 19.1%; Pred. No. 1.3e-09;
Matches 181; Conservative 146; Mismatches 270; Indels 349; Gaps 43;

QY 295 DIVRWTKLLONITSHOH-----LTVYDFEGEGSEELDTVL-----KALVK 336
Db 53 DMPVNRRLQLQRLRHQININCMDEPLGRALLT-AIDNENLEMVELLVMGVETKDALH 111
QY 337 ACKSHSQEPDYDELKALV-----AMDRVDAKSIIFNGDVWKSODLEWVVDALV 389
Db 112 AINAEFVAVELLEHEELLYKEGSPYSOKVDI-NTMFAFDI-----TPMLAAH 162
QY 390 SNKPEFVLFVNDGA--DVADFLTGRLOELVRSYSRSLFDDLQKQEARLTLAGIG 447
Db 163 KNFELILILDLRGAAVVPDHIRG-CEBCVRLTAESL-----RHSLSVN 209
QY 448 TQOAREPP-----AGPAFSLHEYSRVLKD--FLQDACRGFYQDGRPDRAEKPAK 499
Db 210 IYRALCPSLLCLTSDNPIITAFQLSWELRNALATEGCKSEYMD-----LRQCKFAVD 265
QY 500 RPTGKMLLDLNQKSENWRDLFLMAVQNHENATYFMWQGEVAAALAAKLIKEMS 559
Db 266 -----LIDQRTSNE-----LAILIYDPQSSY-----EPG----- 292
QY 560 HLETAABAATREAKYERKALDLFSECYNSSEARAFALVRRNCWSKTTCLHATEAD 619
Db 293 -----DRMSL-----TRVQAISYK 307
QY 620 AKAFPAHDVQAFLTRIWMGDMAACTPILR--LIGAFICPALVYTNLITFSEAPLRIG 676
Db 308 QKKFAHNIQQLSSIYVD--GLPGRRSIYDKVICTAIV--AVLF----- 351
QY 677 LEDLDDLSLDTKSPLYGL-----QSRVELVAPPAQDGRGRAVFLTRMKKFMGA 730
Db 352 -----FLYCLLYMCAPNCRGTQGL-----RK----- 372
QY 721 PVTVELGNVWVFAFLPFLTYLVLY-----DPRPPQSPG 766
Db 373 PFMKFLIHASSYLFPLT--LILVSGRADDDFVRIFGTRMKKLAEOELRQROTBSK 429
QY 767 PEVTLVFWFLVLEIRIGQFETDEDTHLYKKFTLYVGDNNKCDMVAIFLFIYVTCRM 826
Db 430 LELIYVMYVIGFVMEVQEIFAVGMS-----YLRNMNFIIDFLRNSLY-VGVMC-L 479
QY 827 LPSAFEGRTVLAAD-----FMVLT-LRLHIFAIHQOL 859
Db 480 RAFAYIQOATEIARDPQMAVYIPREKMHDPQLIAEGFAANVSAKLVLFISINPL 539
QY 860 GKLIIVRRMKDV--FFELPFLSYMLVAAYGT-----TQALLHPDGLW-- 904
Db 540 GFLQSLGKRWVIDVKEFFIYTLVFAFCGLNQLMTFALEKSKCYLP-GGEADMG 598
QY 905 -----IFRRV--LYRP-----YLQIFGOIPLDEIDAEVNCSTHLLLEDSPSCSLYAN 952
Db 599 HGDSCMKRRRFGNPLESSQSJFWASFVGVGDDPFLSGIKS-----YTR 642
QY 963 WIVILLVTELLVNLVNLMLLIAMFSTFPVOVQGNATFMKFGQYMLIVEHPRP-LA 1011
Db 643 FGLMLFGSYVINIYVNLILMIAMMSNSYAMIDHSPTWFAFTKLMGSEFESATLP 702
QY 1012 PFIILSHSLRLRVFKEKAEHREHLERLDPLDQKVYVWEVQKCNFLSKMEKRR 1071
Db 703 PFENVLPSPKVI-RIFRSS-----KTIIDQSKKREOEQF 739
QY 1072 DSEGVLRKTAHRVDVFIAYLGLREO-----EKRIKLESQIN 1110
Db 740 SEYDNIMR-----SLWRYVAAMRKRENNVSEDDINEVSEIN 779
RESULT 6
TRP2 MOUSE
AC Q9R244; Q9R244; Q9R244; Q9R244; Q9R244; Q9R244; Q9R244; Q9R244; Q9R244; Q9R244;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)

DE Short transient receptor potential channel 2 (trpc2) (mtrp2).
 GN TRPC2 OR TRRP2 OR TRP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Testis;
 RX MEDLINE=99162557; PubMed=10051594;
 RA Vannier B., Peyron M., Boulay G., Brown D., Qin N., Jiang M., Zhu X.,
 RA Birnhauser L.;
 RT "Mouse trp2, the homologue of the human trpc2 pseudogene, encodes
 RT mtrp2, a store depletion-activated capacitative Ca2+ entry channel.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2060-2064(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
 RX PubMed=10998353;
 RA Hofmann T., Schaefer M., Schultz G., Gudermann T.;
 RT "Cloning, expression and subcellular localization of two novel splice
 RT variants of mouse transient receptor potential channel 2.";
 RL Biochem. J. 351:115-122(2000).
 CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. MAY ALSO BE
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=A;
 CC IsoId=Q9R244-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q9R244-2; Sequence=VSP_006562;
 CC Name=3; Synonyms=Alpha;
 CC IsoId=Q9R244-3; Sequence=VSP_006564;
 CC Name=4; Synonyms=Beta;
 CC IsoId=Q9R244-4; Sequence=VSP_006563, VSP_006565;
 CC -1- TISSUE SPECIFICITY: ISOFORM 3 IS UBICUITOUSLY EXPRESSED AT LOW
 CC LEVELS. ISOFORM 4 IS EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 3 ANK repeats.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF111108; AAD17196.1; -;
 CC EMBL; AF111107; AAD17195.1; -;
 CC EMBL; AF230803; AAG29951.1; -;
 CC EMBL; AF230802; AAG29950.1; -;
 CC MGD; MGI:109527; Trpc2.
 CC GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.
 CC GO; GO:0000139; C:Golgi membrane; IDA.
 CC GO; GO:0005635; C:nuclear membrane; IDA.
 CC GO; GO:0015279; F:store-operated calcium channel activity; IDA.
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; IPI.
 CC InterPro; IPR002110; ANK.
 CC InterPro; IPR002111; Cat_channel_TrypL.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR005820; M-channel_nlg.
 CC InterPro; IPR002153; Trans_receptor.
 CC InterPro; IPR005458; TRPChannel2.
 CC InterPro; IPR002706; Xrcc1_N.
 CC Pfam; PF00520; Ion_trans; I.
 CC Pfam; PF01834; Xrcc1_N; I.
 CC PRINTS; PRO1097; TRANSRECEPT.
 CC PRINTS; PRO1643; TRPCHANNEL2.

DR ProDom; PD023136; Xrcc1_N; 1.
 DR SMART; SM00248; ANK; 2.
 DR POSITE; PS50088; ANK_REPEAT; FALSE NEG.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; FALSE NEG.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KM ANK Repeat; Repeat; Alternative splicing;
 FT DOMAIN 1 659
 FT TRANSMEM 660 680
 FT DOMAIN 681 702
 FT TRANSMEM 703 723
 FT DOMAIN 724 738
 FT TRANSMEM 739 759
 FT DOMAIN 760 789
 FT TRANSMEM 790 810
 FT DOMAIN 811 833
 FT TRANSMEM 834 854
 FT DOMAIN 855 899
 FT TRANSMEM 900 920
 FT DOMAIN 921 1172
 FT REPEAT 301 330
 FT REPEAT 377 406
 FT REPEAT 430 459
 FT DOMAIN 1140 1143
 FT VASPLIC 1 111
 FT VASPLIC 2 283
 FT VASPLIC 2 287
 FT VASPLIC 284 287
 FT CONFLICT 628 628
 FT CONFLICT 633 633
 FT CONFLICT 653 653
 FT CONFLICT 774 774
 FT CONFLICT 797 797
 FT CONFLICT 1161 1161
 SQ SEQUENCE 1172 AA; 130467 MW; B6A6F4BB941E946 CRC64;
 Query Match 4.2%; Score 258.5; DB 1; Length 1172;
 Best Local Similarity 20.2%; Pred. No. 2.7e-09;
 Matches 239; Conservative 144; Mismatches 364; Indels 439; Gaps 51;
 QY 161 HYPE--DDGSGG--PLC---SLDSNLSHFLVPEGP--PGKGDGTLRLRLRK 206
 DB 215 HRPQTKSDGGVQAAGCCPLCAGFPFISITLPHQAATCGESPPOBPASPASSSSSVLR 274
 QY 207 HISQORAGYGTGSIETFPVCLLVNCPNPTLERSRAVEQAAPLILVSGGIADVLAAL 266
 DB 275 H-----HVALTPVLPVKPPNMT-----I 295
 QY 267 VNCPHLVPKVAEKQFEKPKFMSWEDIVRWTKLQNTTSHOHLTVYDFEGSGSEL 326
 DB 296 VNK-----KLKFP-----FTLRLAI-----QEGQLG 317
 QY 327 DTVILKLVAKCS-----HSQEPQYLDLKLAVADRVIAKSEIFNGDVWEKS 377
 DB 318 VQQLSESSDPSGAGPGPLRNVEESDRSRREALNIALRIGHVY--TDVILANVKRDF 375
 QY 378 CDLEWVADALVSKPEFVRLFVUNGADVADFLTYGRQ--ELYSVSKSLFLFDLQRKQ 436
 DB 376 RQIHALLVAVDTQOPAVVRRL-----ARLERKGRKRVTKSPSLAFPDSSI 423
 QY 437 EEAR-----LTLAGLGTQOAREPPAGPAFSLHEVSVLKPDLOACRGFYQDGRGDRR 492
 DB 424 DGRFAPGVPITLTAQK-----DIYEIAQLMDQGHITAR-----PHPVSCAC 467
 QY 493 AEKGPARKPTGQKWLILNOKSENPMWRDLFLMAVLQNRHEMATYFMWAGDGVAAALAA 552
 DB 468 LECSNARRYD--LTKFSLSRINTYRGIASRAHLISLSE-----DAMLAALF 510

```

QY 553 KILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAPALL-VRNRCSKTC 611
DB 511 QLSRELRL-----ARKEPEKPOYIALESICDY-----GFELMGCRQ--SEVTA 556
QY 612 -----LHATEADAKAFPAHDGQAFLEIRIMWD 640
DB 557 VLNDGDESETEREABGLQAFEEGIPNARLRALVNVNQKQFVAHPICQVLTSSIMCN 616
QY 641 MA---AGPILALGA-----FLCPALVYTNLTITSEEARPLTGLEDLDDSLDTE 689
DB 617 LAGMRGSTITMRLFVASLIFLTMPLFCIG----- 645
QY 690 KSPFLGQSRVSEIVEAPARAGDRGRAVEFLTRMRKFWGADVTVLGNVNYPAFL-FL 748
DB 646 ---YWL-----APKSO-----LGRLLKI--PVLKFLHSASYLWFLFL 679
QY 749 FTYVLLVD-----FRPPQSGSGPEVTVL-FWVFTLVLEIRQGFPTDEDTHLVKKFTLY 802
DB 680 LGESLVMETQSTFKGRSQ--SVWETSJHMIVWTGTLMECKEVM-----IEGLREY 729
QY 803 VQDNMKKCDMAIFLFTV-----GVTCRMILPSAFEA----- 833
DB 730 LIDMWNFLDVVILSLYLASFALRLLAGLAVMHCBDASDSTCRCPFTTERSEWRTEDQ 789
QY 834 --GRVTLAMDVWFTLRHLHFAHKGQKPIIVERMKKQVFFFLFSLVWLVAVGVT 891
DB 790 FLAEVLFVTSMLSTRFLAYILPAHESLGTLOISIGKMDMIRFVILMITLTAFLCL 849
QY 892 QALLPHD-----GRLEWIFRRVLYKPYLQIFQOIPLDEIDEARVNCSTHPLLEDSPSC 946
DB 850 NNIVYVQSEKLGNNENFQFLW-----TWFGMEHVTVD-----MPQFLVEBFG 897
QY 947 PSLYANWLVLLVFLVLTNVLLNMLLAMSSTYTOVQGNATMFKQRNLVLEY-H 1005
DB 898 RMYGIFTVWVIV-----LNMILTAMITNSFOKIEDADVWFKRSKLYLSYER 948
QY 1006 EEPALAPFLTLSHSLT---LRVFK-----KEA 1032
DB 949 EGLTLPVPNNILPSPAAYLVRLIFPLCCSSCKAKKSDYPPGTITNGARAGSAG 1008
QY 1033 EHKREHLERDLDPDLQKVTVETWQENFLSMKERRRDSGEVLKTAHVRDFTAKYL 1092
DB 1009 EGERVSYRRLVKALVQRYI--ETARE-----FEETR--KOL 1043
QY 1093 GG-LRQERIKLCLESQINYCVLSVADVLAQGGEP-----SSQH 1134
DB 1044 GRLTELTKTVSLQSE-----VASVQKNLAAAGAPRPDASILSRVITRVNSFQ 1096
QY 1135 CGEGSQLVADHR-----GGIDGWBQGA---GPPSDT 1165
DB 1097 LGPPTSDTPAELTMPEIVETEVS LGDLDTGEGANGAPAGEPSSS 1142

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 96:5791-5796(1999).
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED CALCIUM PERMEANT
CC CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL
CC SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR
CC G-PROTEIN COUPLED RECEPTORS. IS NOT ACTIVATED BY INTRACELLULAR
CC CALCIUM STORE DEPLETION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (probable).
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN
CC NEURONS (SENSORY MICROVILLI).
CC -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 3 ANK repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AF136401, AAD31453.1, -.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR002111; Cat_channel_Trl.
CC InterPro: IPR005821; Ion_trans.
CC InterPro: IPR005820; M-channel_nlg.
CC InterPro: IPR002153; Trans_receptor.
CC InterPro: IPR005458; TRPchannel2.
CC Pfam: PF00023; ank; 2.
CC Pfam: PF00520; Ion_trans_1.
CC PRINTS: PR01097; TRANSRECEPRP.
CC PRINTS: PR01643; TRPCHANNEL2.
CC SMART: SM00248; ANK; 3.
CC PROSITE: PS50068; ANK_REPEAT; FALSE NEG.
CC PROSITE: PS50297; ANK_REPEAT_REGION; FALSE NEG.
CC Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC ANK repeat; Repeat.
CC KW
CC FT DOMAIN 1 375 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 376 396 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 397 418 POTENTIAL.
CC FT TRANSMEM 419 439 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 440 454 POTENTIAL.
CC FT TRANSMEM 455 475 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 476 505 POTENTIAL.
CC FT TRANSMEM 506 526 POTENTIAL.
CC FT DOMAIN 527 549 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 550 570 POTENTIAL.
CC FT DOMAIN 571 615 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 616 636 POTENTIAL.
CC FT DOMAIN 637 885 CYTOPLASMIC (POTENTIAL).
CC FT REPEAT 17 46 ANK 1.
CC FT REPEAT 93 122 ANK 2.
CC FT REPEAT 146 175 ANK 3.
CC FT DOMAIN 853 858 POLY-SER.
CC SQ SEQUENCE 885 AA; 99611 MW; BA23F87F2BEFAF85 CRC64;

Query Match 4.0%; Score 244; DB 1; Length 885;
Best Local Similarity 21.2%; Pred. No. 1.7e-08;
Matches 192; Conservative 121; Mismatches 301; Indels 290; Gaps 37;

QY 344 EPODYDELKLAVANDRVDAIKSEIFNGDVEKSCDLEWVDALVSNKPEFRLFVNDG 403
DB 60 EDRSWREANLALIRLGHEVI--TDVILANVKEDPQIHALLAVDVTNGPAVVRLL--- 114
QY 404 ADVADFLTYGRIC-ELYRSVSKSLFDLLQKQEBAR---LTLAAGCTQQAAREPPAGP 458
DB 115 -----ARLEREKGRKVDTKSFLAFDSDSISGSRAPAVTPLLACQK----- 157
QY 459 PAFSLHEVSRVVKDPLQDAGRFGYODGRGRARRAKGAPKPTQKWLIDNQSSENP 518
DB 158 ---DIYEALQLLMDGHTTAR-----PBPVSACLECSNARYD---LLKFSLSRINTY 205
QY 519 RDLFLWAVLQNHMAVTFWAMGQEGVAALAAKILKEMSHLETEAARATREAKYER 578

```

RESULT 7
TRP2 RAT
ID TRP2 RAT STANDARD; PRT; 885 AA.
AC Q9R283;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 2 (Trp2) (Trp2).
GN TRP2 OR TRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99254120; PubMed=10318963;
RX Litan E.R., Corey D.P., Dulac C.;
RT "TRP2: a candidate transduction channel for mammalian pheromone
sensory signaling.";

```

Db      206 RGIARAHSLASE-----DMTLAFLUSRELR-----ARPEPFKQY 246
Qy      579 LALDFSECYNSSEARAFALL-VRNRCSKTT-----611
Db      247 IALSELCDY-----GPELLGMCNQ--SEVTAVLNDGSESEPEAEGLQAFEECI 298
Qy      612 ----LHATEADAKAFPAHDGVQAFTRIMWGDMA--AGTRILLGALFCFALVYTN 663
Db      239 PNLARLRVAVNYNQKQFVAHPICQOVLSIMCGNLAGMRGTTIWLFFVAFILF-LTWP 357
Qy      664 LITFEBAPIRTGLDLDLSDLTREKSLVGLQSRVETLVAPRAQGRGPAFLTR 723
Db      358 LCTGYWLP-----KSRLLGLK-----375
Qy      724 WRKFWGAPVTVFLGNVVMYFAFL-FLFTYVLVD-----FRPPQSGSEVTLV-FWVF 776
Db      376 ----IVLKLHLHSASTLWFLIFLGLSELVMEQLSTFKRSQ--SWETSILMIVYT 427
Qy      777 TLVLEIRGQFTDEDTHLVKKFTLVYGDNNKCDMVALFLPIGV-----822
Db      428 GFLMECKEVM-----IEGLRSYLLDMNFDVILSTVLASFALRLLAGLAWMC 479
Qy      823 ----TCRMLPSAFEA-----GRVLANDFNVFTRLHIFPAIKQLGPKIIV 865
Db      480 RDASDSSTCRYFTTARSEMRTEDEPLAEVLFVAVTSMLSFTRLAYILPAHESLGLQIS 539
Qy      866 VERMMKQVFFLFLFVSVMLVAVGVTTOALLHPD-----GREWAFRRVLYAPYQIQG 920
Db      540 IGMKMDMIRFWMILMITLTAFLCGLNNIYVYQETELKNENETFOFQFV---TWGMC 595
Qy      921 IFLDEIDARVNCSTHPLLEDSPSCPSLYANMLVLLVFLVTLVNLMLLJAMESY 980
Db      596 EESHVVD-----MPGLVPEFVGAMYGIFITVIV-----LMLMLAMTIN 638
Qy      961 TPQVQGNATMFKQRYNLVLEY-HERPALAPPTILSHSLT---LRV-----1028
Db      639 SFQKIEDADVEMKPARSKLYSYREGLTLPVPNNILPSPKAFVLLRRIRPFCGSS 698
Qy      1029 ----KKE-----AEHKREHLERDLPDLQKVVTWQENFLSKME 1067
Db      699 CCKAKKSYPIPTTNGEARGPGEVSVRLRYITALVQRYI--ETARE-----FE 751
Qy      1068 KRRDSEGEVLKTAHRYDIFAKYIG--LRQEKIKICSQINCSVLYSSVADVLQ 1126
Db      752 ETRR-----KDLGNRLTELTKVSRQSB-----VASQKTVAG 786
Qy      1127 GQPR 1130
Db      787 GALR 790

```

RESULT 8
TRPL_CAEEL
ID TRPL_CAEEL STANDARD; PRT; 1027 AA.
AC P34586; P34585; O81G03;
DT 01-FEB-1994 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transient-receptor-potential like protein (TRP homologous cation channel protein 1).
GN TRP-1 OR STRPC1 OR ZC21.2/ZC21.1.
OS Caenorhabditis elegans.
OC Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditya; Metazoa; Nemtoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditya; Metazoa; Nemtoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditya; Metazoa; Nemtoda; Chromadorea; Rhabditida; Rhabditoidea;
OK NCBI_taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Hareneck C.; Schultz G.;
RT "Cloning and functional expression of C. elegans TRP isoforms";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBS databases.
RN [2]
RP SEQUENCE FROM N.A.

```

RC STRAIN-Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almsough R., Anderson K., Baynes C., Berke M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Suleston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
RN [3]
RP REVISIONS.
RA Waterson R.;
RL Submitted (DEC-2002) to the EMBL/Genbank/DBS databases.
CC -1- FUNCTION: COULD MEDIATE CALCIUM ENTRY AND FORM A CALCIUM PERMEANT
CC CHANNEL (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY, STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 3 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sb.ch/announce/
CC or send an email to license@isb-sb.ch).
CC -----
CC EMBL: AJ276027; CAC81654.1; -
CC EMBL: L16685; AA28167.3; -
CC WormPep; ZC21.2; CE33009.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR002111; Cat_channel_TrpL.
CC InterPro: IPR005821; Ion_trans.
CC InterPro: IPR002153; Trans_receptor.
CC Pfam: PF00023; ank; 2.
CC Pfam: PF00520; ion_trans; 1.
CC PRINTS: PR01097; TRANSRECEPT.
CC SMART: SM00248; ANK; 2.
CC TIGRFAMs: TIGR00870; trp; 1.
CC PROSITE: PS50088; ANK_REPEAT; 1.
CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
CC Hypothetical protein; Ionic channel; Transmembrane; Ion transport;
CC ANK repeat; Repeat.
CC ANK repeat; Repeat.
CC TRANSMEM 355 375 POTENTIAL.
CC TRANSMEM 391 411 POTENTIAL.
CC TRANSMEM 473 493 POTENTIAL.
CC TRANSMEM 516 536 POTENTIAL.
CC TRANSMEM 559 579 POTENTIAL.
CC TRANSMEM 640 660 POTENTIAL.
CC REPEAT 85 115 ANK 1.
CC REPEAT 117 141 ANK 2.
CC REPEAT 153 192 ANK 3.
CC SEQUENCE 1027 AA; 118101 MW; E1B83635A5DE2PAD CRC64;

```

Query Match 3.9%; Score 239; DB 1; Length 1027;
Best Local Similarity 19.5%; Pred. No. 4.5e-08;
Matches 134; Conservative 109; Mismatches 234; Indels 210; Gaps 25;
Qy 549 LAACKIKEMSHLETEAARAT--REAKYERLALDFSECYNSSEARAFALLVRRNR- 604
Db 240 LSAFLSMDLQRLAFEEHEFETLYLQSECKQYSCDLSGCRSSSE--VAILNKGNV 297
Qy 605 ----CWS---KITCLHATEADAKAFPAHDGVQAFTRIMWGDMAAGTFLRLGAF 655

```

Db 298 NDNNDIVAMSKLSRLKLAIEQKAFVSHPHCOOLLTSIYW-----ESIPYRORSGTWA 353
Cc 656 CFALVYTNLTITSEEARPLATGLEDQDDLSLSTKESPLVGL-----GSRVELLEAPRA 709
Db 354 NEFLAFLFLM-----PIFCMLTILMPKSRGLRVRSP-- 387
Cc 710 QCDRGPRAFVLLTRMKFVGADPVFLGNVVMYFAVLFPLFTVLLVDF-----R 758
Db 388 -----FMKFFYYSVS-----FATFLGLLTATPEFDVYEKGEKGMTR 425
Cc 759 PPPQSGSP--EVLTYFWVFLVLEIRGQFTDEDTLVKKFTLYGVGNMKNKCMVAIF 816
Db 426 ASDRGPRATWVESLVFTWVIGMLMSEIKQLM-----EEGFKRYMRQMMWMLFLMIC 477
Cc 817 LEIVGTCMMLPSAPF-----AARTVAMQFWFTLRILHI 852
Db 478 LVLCTISLNL--SAYITFYREDPRYRYVTWTSEEPMLVADALFAVGNVNSFAIITL 535
Cc 853 FAIHKQLGPKIIVVERMKDVFPLFLFSLVWLVAVGVTYQALLPHPDGRLEWIFRVLXR 912
Db 536 FQTNVYLGPIQLSLGCMVLDVAKFCIFVLIISSPSIGLAQLWYVDPTDCLPGATCK 595
Cc 913 PYLQIFGQIPDEIDEARVNCSTHPLL-----EDSPSCPS-LVANMLVILLVTF 962
Db 536 HSNVFFSSI-----ADSYLTILWLSFSTKPEDTDVVENHKITQWVGQGFIMY 644
Cc 963 LLVTNVLNLLIAMSTYFOVVGQATMFKFORNL-IVEYHERPALAPF-ILSLTL 1020
Db 645 HCTSIIVLLNMLIAMSHSFQIINHADLEWKFHRTKLMAMHFDDESSLPPEFNIIIVTK 704
Cc 1021 SL-----TLRVFKKEA-----EHKREHLER-----DLPPPLDQK 1050
Db 705 SLIYVNCLEFNIVRMILGKYTKYQKNRATIRPGSRGRNEMKSGCHDDSLKPLTYA 764
Cc 1051 VVTWETVQ-----KENFLSKMEKRRDSEGVLRKTAHVRDF 1087
Db 765 DIITRLVAFIRHQTCKMDKMGVNEEDLHEIKODISSLRLEYLRDREIRVSSSH-IDA 823
Cc 1088 IAK-----YLGSLRQEKER 1101
Db 824 VRDIDIRMTSTTSRRPFGSMPLPKTR 850

```

RESULT 9

TRP5_HUMAN STANDARD; PRT; 973 AA.

AC Q9UL62; O75233; Q9Y514;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Short transient receptor potential channel 5 (TRPC5) (Htrp-5) (Htrps).

GN TRPC5 OR TRP5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RX MEDLINE=99425273; PubMed=10493832;

RA Sossage-Alaoui K., Lyon J.A., Jones L., Abidi F.E., Hartung A.J.,

RT "Molecular cloning and characterization of TRPC5 (HTRP5), the human

RT homologue of a mouse brain receptor-activated capacitative Ca(2+)

RT entry channel.";

RT Genomics 60:330-340(1999).

RL [2]

RP SEQUENCE FROM N.A.

RA Rohlfing T., Langston Y., Mead K., Bird C.;

RL Submitted (JUN-1998) to the EMBL/Genbank/DBD databases.

CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE

CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A

CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR

```

Cc 1 TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
Cc 2 SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
Cc 3 ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
Cc 4 -!- SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
Cc 5 -!- SUBCELLULAR LOCATION: Integral membrane protein (probable).
Cc 6 -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN WITH HIGHER LEVELS IN FETAL
Cc 7 BRAIN.
Cc 8 -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY, STRPC
Cc 9 SUBFAMILY.
Cc 10 -!- SIMILARITY: Contains 2 ANK repeats.
Cc 11 -----
Cc 12 This SWISS-PROT entry is copyright. It is produced through a collaboration
Cc 13 between the Swiss Institute of Bioinformatics and the EMBL outstation
Cc 14 at the European Bioinformatics Institute. There are no restrictions on its
Cc 15 use by non-profit institutions as long as its content is in no way
Cc 16 modified and this statement is not removed. Usage by and for commercial
Cc 17 entities requires a license agreement (see http://www.isb-sib.ch/announce/
Cc 18 or send an email to license@isb-sib.ch).
Cc 19 -----
Cc 20 EMBL, AF054568; AAF00002.1; -
Cc 21 EMBL, AC005191; AAC24563.1; -
Cc 22 EMBL, AL049563; CAB44737.1; -
Cc 23 Genew, HGNC:12337; TRPC5.
Cc 24 MIM, 300334; -
Cc 25 GO, GO:0005887; C:integral to plasma membrane; TAS.
Cc 26 GO, GO:0015279; F:store-operated calcium channel activity; TAS.
Cc 27 GO, GO:0006816; P:calcium ion transport; TAS.
Cc 28 GO, GO:0007399; P:neurogenesis; TAS.
Cc 29 InterPro, IPR002110; ANK.
Cc 30 InterPro, IPR002111; Cat_channel_Tyrl.
Cc 31 InterPro, IPR005821; Ion_trans.
Cc 32 InterPro, IPR002153; Trans_receptor.
Cc 33 InterPro, IPR004729; Trp_CaChannel.
Cc 34 InterPro, IPR005461; TrpChannels5.
Cc 35 Pfam, PF00023; ank; 2.
Cc 36 Pfam, PF00520; Ion_trans; 1.
Cc 37 PRINTS, PRO1097; TRNSRRECEPTR.
Cc 38 PRINTS, PRO1646; TRPCCHANNELS.
Cc 39 SMART, SM00248; ANK; 2.
Cc 40 TIGRFAMs, TIGR00870; trpf_1.
Cc 41 PROSITE, PS50088; ANK_REPEAT, FALSE NEG.
Cc 42 PROSITE, PS50297; ANK_REPEAT_REGION, FALSE NEG.
Cc 43 Ionic channel; Transmembrane; Ion transport; Calcium channel;
Cc 44 ANK repeat; Repeat; Glycoprotein.
Cc 45 KW
Cc 46 DOMAIN
Cc 47 1
Cc 48 330
Cc 49 CYTOPLASMIC (POTENTIAL).
Cc 50 FT TRANSMEM 331 351
Cc 51 FT DOMAIN 352 398
Cc 52 FT TRANSMEM 399 419
Cc 53 FT DOMAIN 420 437
Cc 54 FT TRANSMEM 438 458
Cc 55 FT DOMAIN 459 470
Cc 56 FT TRANSMEM 471 491
Cc 57 FT DOMAIN 492 512
Cc 58 FT TRANSMEM 513 533
Cc 59 FT DOMAIN 534 603
Cc 60 FT TRANSMEM 604 624
Cc 61 FT DOMAIN 625 973
Cc 62 FT REPEAT 69 98
Cc 63 FT REPEAT 141 170
Cc 64 FT SITE 971 973
Cc 65 FT CARBOHYD 461 461
Cc 66 FT SEQUENCE 973 AA; 111411 MW; F8C8BFL17B842166 CRC64;
Cc 67

```

Query Match

Best Local Similarity 21.5%; Score 231; DB 1; Length 973;

Matches 140; Conservative 97; Mismatches 232; Indels 182; Gaps 28;

QY 555 LKEMHLETEAFAAATREAKYERLALFLSCYNSSEARAFALVRN-----RCW 606

DB 227 LKELSKVNEFAEYEEELISQCKLPAKLLDARSSREI--ILNHRDDHSEELDPQY 284

QY 607 SKTCLHLATEADAKAFPAHDGVQAFRLRIWGDWAAGTP-----ILRLIGAFLCFAL 659

```

Db 285 HDLAKLKAIAKHQEFVAQPNCCQLLATLWYD-----GPPGRRKRWVKLL---TCMTI 337
Qy 660 VYTNLTISESEAPRLRTGLEDLDLSDLTESKPLYGLOSREVELVEAPRAQDGRPAV 719
Db 338 GF-----LFPMLSTAYLISPRNL---GL----- 358
Qy 720 LITMRKFWGAPVTVFLGNVWVYFAFLFLF---TYVLVDFRPPPGSGPEVTLVFW 775
Db 359 -----FIKKPFIKFICHTASVTLFLFMLLASQHVIRTDHVQGPPTVEMMLPMV 411
Qy 776 FTVLVEIRQ---GFTDEDTLHVKKFTLVYGDNNKCDMAVFLFVGTCTMLPSAFE 832
Db 412 LGFIMGEIKEMWDGFT-----YIHDWMNMDPMANNSLYLATISLKIYAVYKY 460
Qy 833 AG-----RTVLAMPVFTLRLIHIPIAHKQIGKTIIVERMMQDVFF 876
Db 461 NGSRRREWEKMHPTLIALFAINISLSLISLFTANSHLGPLQISLGMLDILKF 520
Qy 877 LFFLSVWLAVG-----VTTQALLPH-----DGRLEWIFRVLVYRPIQI 917
Db 521 LFYCLVLLAFANGNLQYFYETRAIDEPNNCKGIRCEKONNASTLF-ETLQSLFWSV 579
Qy 918 FGQIPLDEID-EARVNCSTHPLLEDSPSCSGLYANMLVILLITVLLVNLMLIIA 976
Db 580 FGLNLVYTNVYAR-----HE-----FTEFGVATMFGYVNIISLVLLMLIA 622
Qy 977 MESYTFVQVGNATWFMKFORNLVLEY-HERPALAPP-LLSHLS-LTLRVPKKA 1033
Db 623 MANNVQLADHADIEKFAKTKMWSYFDEGTLPPPNIIIPSKFLYLGNNMNTFC 682
Qy 1034 HKREHLERDLPDLPDQVTVETVOKENFLSKMERKRRDS-----EGEVLRTKHARVDF 1087
Db 683 PKRD-----PDGR-----RRRNLSFTERNADSLIQNHQVYERINLVKR--Y 724
Qy 1088 IA-----KYGGLREOE-KAIKCLSEQINYSVLVSSVADYLAQGGPRS 1131
Db 725 VAAMIRNSKTHGELTEENFEKELKODISSFRY-----EVLDLGNRKAPRS 769

RESULT 10
TRPS_RABIT STANDARD; PRT; 974 AA.
AC 062852;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 5 (TRPC5) (Rtrps)
GN TRPC5 OR TRPS.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98353453; PubMed=9687496;
RA Philipp S., Hambrecht J., Braelavak L., Schroch G., Freichel M.,
RA Murakami M., Cavallie A., Flocke V.;
RT "A novel capacitative calcium entry channel expressed in excitable
RT cells."
RL EMBO J. 17:4274-4282 (1998).
CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC THROSN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY
CC INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. TRPC

```

```

CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, AJ006203, CAA06911.1, -.
CC InterPro: IPR002110, ANK.
CC InterPro: IPR002111, Cat_channel_Tryp.
CC InterPro: IPR005821, Ion_trans.
CC InterPro: IPR002153, Trans_receptor.
CC InterPro: IPR004729, Trp_Channel.
CC InterPro: IPR005461, TrpChannel15.
CC Pfam: PF00023, ank. 2.
CC Pfam: PF00520, Ion_trans. 1.
CC PRINTS: PR01097, TRANSRECEPT.
CC PRINTS: PR01646, TRCHANNELS.
CC SMART: SM00248, ANK. 2.
CC TIGRFAMs: TIGR00870, trp. 1.
CC PROSITE: PS50088, ANK_REPEAT; FALSE NEG.
CC PROSITE: PS50297, ANK_REPEAT_REGION; FALSE NEG.
CC K1 Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC ANK repeat; Repeat; Glycoprotein.
CC DOMAIN 1 330
CC TRANSSEM 331 351
CC FT TRANSSEM 352 398
CC FT DOMAIN 399 419
CC FT TRANSSEM 420 437
CC FT DOMAIN 438 458
CC FT TRANSSEM 459 470
CC FT DOMAIN 471 491
CC FT TRANSSEM 492 512
CC FT DOMAIN 513 533
CC FT TRANSSEM 534 603
CC FT TRANSSEM 604 624
CC FT DOMAIN 625 974
CC FT REPEAT 625 974
CC FT REPEAT 141 170
CC FT DOMAIN 690 693
CC FT SITE 972 974
CC FT CARBOHYD 461 461
CC FT SEQUENCE 974 AA; 111536 MW; 94256B0F28925316 CRC64;

Query Match 3.88; Score 231; DB 1; Length 974;
Best local similarity 21.58; Pred. No. 1.4e-07;
Matches 140; Conservative 98; Mismatches 232; Indels 182; Gaps 28;

Qy 555 LKEMSHLETEAEARATREAEYERLALDLFSECSNSEARAFALLVRRN-----RCW 606
Db 227 LKELSKYENKAEYELSSQCKLFAKDLDDQARSSRELE--ILNRDHSSELDPOKY 284
Qy 607 SKTTCILHATEADAKAFADHDGVAFLTRIMWGMAAGTP-----ILRLGAFLCFAL 659
Db 285 HDLAKLKAIAKHQEFVAQPNCCQLLATLWYD-----GPPGRRKRWVKLL---TCMTI 337
Qy 660 VYTNLTISESEAPRLRTGLEDLDLSDLTESKPLYGLOSREVELVEAPRAQDGRPAV 719
Db 338 GF-----LFPMLSTAYLISPRNL---GL----- 358
Qy 720 LITMRKFWGAPVTVFLGNVWVYFAFLFLF---TYVLVDFRPPPGSGPEVTLVFW 775
Db 359 -----FIKKPFIKFICHTASVTLFLFMLLASQHVIRTDHVQGPPTVEMMLPMV 411
Qy 776 FTVLVEIRQ---GFTDEDTLHVKKFTLVYGDNNKCDMAVFLFVGTCTMLPSAFE 832
Db 412 LGFIMGEIKEMWDGFT-----YIHDWMNMDPMANNSLYLATISLKIYAVYKY 460

```

```

OY 833 AG-----RTVLAMFVETLRLIHFAIKHQLGPKIIVERMMKDVFF 876
DB 461 NCSRRREWEWMHPTIALALFAISNLSLISLFTANSHPGLQISGLMDLIXF 520
OY 877 LFFLSVWLVAAG-----VTTOALLHPH-----DGRLEWIFRRVLYRPILOI 917
DB 521 LFVYCVLLAFANGLNQLFYFVETRAIDEPNCKGRCCKONNAFTFL-ETLQSLFMSV 579
OY 918 FQOIPLEID-BAFVNCSTHPLLEBSPCBLVXNWLVLILLVPLVTLNVLNMLLIXF 976
DB 580 FGLNLVYTVNVAR-----HE-----FEEVGATMGTYNVLVLLMLLIXF 622
OY 977 MESYFQVQVGNATVFWKFORYNLVEY-HERPALAPF-ILSLHS-LTLRVEFKAE 1033
DB 623 MWNNSYQLADHADIEMKFAFKLMSYRDEGTLPPENIIPSPKFLYLGWFWNTFC 682
OY 1034 HKREHLERDLPPLDOKVTVTWETVCKENFLSKMKERRDS-----EGVLKRTAHRVDF 1087
DB 683 PKRD-----PDGR-----RRNHLRSFTEHRLADSLIONGHYCEVHNLVLR--Y 724
OY 1088 IA-----KYLGLRPOE-KRIKLESQINYSVLSVADVLACGGGRSS 1132
DB 725 VAMIRNSKTNEGTLTEENFKELKODISSFRY-----EVLDDLGNRKQPRRS 770

RESULT 11
TRPS_MOUSE STANDARD; PRT; 975 AA.
ID TRPS_MOUSE
AC Q9QX29; Q61059; Q9QWT1; Q9ROD4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short Transient receptor potential channel 5 (TRPC5) (Transient
receptor protein 5) (Mtrp5) (trp-related protein 5) (Capacitative
calcium entry channel 2) (CCE2).
GN GN TRPC5 OR TRP5 OR TRP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98221157; PubMed=9553080;
RA Okada T., Shintzu S., Wakamori M., Maeda A., Kurosaki T., Takada N.,
Imoto K., Mori Y.;
RT "Molecular cloning and functional characterization of a novel
RT receptor-activated TRP Ca2+ channel from mouse brain.";
RL J. Biol. Chem. 273:10279-10287(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20545496; PubMed=10980202;
RA Tang Y., Tang Y., Chen Z., Trosc C., Flockerzi V., Li M., Ramesh V.,
Zhu M.X.;
RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ
RT domain-containing protein, NHERF.";
RL J. Biol. Chem. 275:37559-37564(2000).
RN (4)
RP SEQUENCE OF 1-966 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98353453; PubMed=9687496;
RA Philipp S., Hambrecht J., Braslavski L., Schroth G., Freichel M.,
Muller M., Cavaliere A., Flockerzi V.;
RT "A novel capacitative calcium entry channel expressed in excitable
RT cells.";
RL EMBO J. 17:4274-4282(1998).
RN (5)
RP SEQUENCE OF 515-637 FROM N.A.

```

```

RX MEDLINE=96234226; PubMed=8646775;
RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
RA Birbaumer L.;
RT "trp, a novel mammalian gene family essential for agonist-activated
RT capacitative Ca2+ entry.";
RL Cell 85:661-671(1996).
CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY
CC INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN. VERY LOW LEVELS DETECTED
CC IN LIVER KIDNEY TESTIS, AND UTERUS.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@ib-6ib.ch).
CC -----
DR EMBL, AF029983; AAC13550.1; -
DR EMBL, AF060107; AAF02200.1; -
DR EMBL, AJ006204; CAA06912.1; -
DR MGI, MGI:109524; Trpc5.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR002153; Trans_receptor.
DR InterPro: IPR004729; Trp_CaChannel.
DR InterPro: IPR005461; TRPChannels.
DR Pfam, PF00023; ank; 2.
DR Pfam, PF00520; ion_trans; 1.
DR PRINTS, PRO1097; TRANSRECEPTR.
DR PRINTS, PRO1646; TRPCHANNELS.
DR SMART, SM00248; ANK; 2.
DR TIGRFAMs, TIGR00870; trp; 1.
DR PROSITE, PS50088; ANK_REPEAT; FALSE NEG.
DR PROSITE, PS50297; ANK_REPEAT; FALSE NEG.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Glycoprotein.
FT DOMAIN 1 330
FT TRANSMEM 331 351
FT DOMAIN 352 398
FT TRANSMEM 399 419
FT DOMAIN 420 437
FT TRANSMEM 438 458
FT DOMAIN 459 470
FT TRANSMEM 471 491
FT DOMAIN 492 512
FT TRANSMEM 513 533
FT DOMAIN 534 603
FT TRANSMEM 604 624
FT DOMAIN 625 975
FT REPEAT 69 98
FT REPEAT 141 170
FT DOMAIN 630 693
FT SITE 971 973
FT CARBOHYD 461 461
FT SEQUENCE 975 AA; 111457 MW; DF9248168D3D2D62 CRC64;
Query Match 3.8%; Score 231; DB 1; Length 975;
Best Local Similarity 21.5%; Pred. No. 1.5e-07;
Matches 140; Conservative 98; Mismatches 232; Indels 182; Gaps 28;

```

```

QY 555 LKEMSHLETEABARATREAKYERLALLFSECYSNSARAPALLVRN-----RCW 606
D 227 LKELSKYENFEKAEYEELSOOCKLFAKDLDOARSSRELE--ILNHRDHDSEELDPQKY 284
QY 607 SKTCLHATEADAKAFFAHGVQAFLRIMWGDMAATP-----ILRLGAFLCAL 659
D 285 HDLAKLKAITYHOEFAVQAPNCQQLTLTWYD-----GFGMRKRWVVKLL--TCMTI 337
QY 660 VYTNLITFSEBAPLRTGLDLDLDDLTDEKSPLYGLQSRVELEAPRAQDRPRAVF 719
D 338 GF-----LPMNSTAYLSPRSNL--GL-----358
QY 720 LITMRKMGAPVTVFLGNVVMYFAFLF-----TYVLLVDFRPPGSGEVTLYFWV 775
D 359 -----FIKRPFIKFIHTASYLFLFMLLASQHIVRTDLHVQPPFVEMWILPMV 411
QY 776 FTVLVEERQ---GFETDEBTHLVKKFTLYVGDNNKCDMAIPLFYGVTCRMLPSAFE 832
D 412 LGFTWGEIKEMWDGGFTS-----YHDMWNLMDFMANSLSYLTATISLKVAVYKY 460
QY 833 AG-----RTVLANDFMVFTLRLIHIFAIHKQIGPKIIVERMKQVPEF 876
D 461 NGSRPREMEMMHTPLIAEALFALSNILSLRLSLFTANGHGLPQJSLGRMLDIK 520
QY 877 LFLISWLVAVG-----VTTQALLPH-----DGLLEWIFRRVLYRPLYQI 917
D 521 LFIYCLVLLAANGINQLYFYETFRALDEPNCKIGRCEKONNAPSTLF-ETLQSLFMSV 579
QY 918 FGQPLBLDID-EARVNCSTHPLLEDSRCSGLVANNVILLVLYLLVTVNLLMLLIA 976
D 580 FGLNLVYTNVKAR---HE-----FEEFGATMFGYVNIISLVLLMLMIA 622
QY 977 MFSYTFQVQGNATFMFKFORYNLIVEY-HERPALAPF-ILLSLHS-LTLRVPKKEAE 1033
D 623 MANNYSQIADHADDEWKFATKLMASFDEGGITLPPFNIIIPSKSLYLGNFNNFTFC 682
QY 1034 HKREHLERDLPPDLQKVVTWVOKENFLSKMEKRRDS-----EGEVLKRTAHYDF 1087
D 683 PKRD-----PDGR-----RRRNHLASFTRHADSILQNHQYEVIRNLVKR--Y 724
QY 1088 IA-----KYLGLRERD-KRIKLESQINCSVLVSVAVYLAQGGPRSS 1132
D 725 VAAIRMSKTNEGLTEENFKELKODISSFRY-----EVLDLLGNRKAPRRS 770

RESULT 12
TRP4_BOVIN STANDARD: PRT: 981 AA.
AC P79100;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short transient receptor potential channel 4 (TRPC4) (Capacitative
calcium entry channel 1) (CCE1).
GN TRPC4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NC NCB1_taxid=9913;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Adrenal gland, and Retina;
RX MEDLINE=97102798; PubMed=8947038;
RA Philipp S., Cavalie A., Freichel M., Wissenbach U., Zimmer S.,
RT "A mammalian Capacitative calcium entry channel homologous to
RL Drosophila TRP and TRPL.";
RL EMBO J. 15:6166-6171 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC TISSUE=Adrenal gland;
RX MEDLINE=98158580; PubMed=9498815;

```

```

RA Freichel M., Wissenbach U., Philipp S., Flockerzi V.;
RT "Alternative splicing and tissue specific expression of the 5'
RL truncated bCCE1 variant bCCE1delta514.";
RL FEBS Lett. 422:354-358 (1998)
CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY
CC INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: ISOFORM ALPHA ASSOCIATES WITH INOSITOL-1,4,5-TRIPHOSPHATE
CC RECEPTOR (ITPR). INTERACTS WITH NHERF (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=p79100-1; Sequence=Displayed;
CC Name=Beta; Synonyms=Delta 514;
CC IsoId=p79100-2; Sequence=VSP_006566;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLAND. LOWER EXPRESSION
CC IN HEART AND RETINA. ALSO EXPRESSED IN TESTIS. THE SHORT ISOFORM
CC IS SPECIFICALLY EXPRESSED IN THE ADRENAL GLAND.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X9792; CA68125.1; -
CC EMBL; AJ224862; CA112161.1; -
CC InterPro: IPR002110; ANK.
CC InterPro: IPR002111; Cat_chan_TrpL.
CC InterPro: IPR005821; Ion_chan.
CC InterPro: IPR002153; Trans_receptor.
CC InterPro: IPR004729; Trp_CatChannel.
CC InterPro: IPR005460; TRPChannel4.
CC Pfam; PF00023; ank; 2.
CC Pfam; PF00520; Ion_trans; 1.
CC PRINTS; PR01097; TRNSRECEPTR.
CC PRINTS; PR01645; TRPCANMEL4.
CC SMART; SM00248; ANK; 2.
CC TIGRFAMs; TIGR00870; trp; 1.
CC PROSITE; PS50088; ANK_REPEAT; 1.
CC PROSITE; PS50297; ANK_REPEAT_REGION; 1.
CC KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC ANK repeat; Repeat; Alternative splicing.
CC DOWAIN 1 331
CC DOWAIN 1 332
CC DOWAIN 332 352
CC DOWAIN 352 364
CC DOWAIN 364 385
CC DOWAIN 385 438
CC DOWAIN 438 459
CC DOWAIN 459 471
CC DOWAIN 471 492
CC DOWAIN 492 513
CC DOWAIN 513 534
CC DOWAIN 534 601
CC DOWAIN 601 622
CC DOWAIN 622 681
CC DOWAIN 681 712
CC DOWAIN 712 724
CC DOWAIN 724 781
CC SITE 979 981
CC VARSPLIC 1 513

```

ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
 (BY SIMILARITY).
 Missing (in isoform Beta).
 /FtId=VSP_006566.

SQ SEQUENCE 981 AA; 112531 MW; 57B172FD65B791C9 CRC64;
 Query Match 3 6%; Score 221; DB 1; Length 981;
 Best Local Similarity 19.6%; Pred. No. 6.9e-07;
 Matches 153; Conservative 105; Mismatches 241; Indels 282; Gaps 31;
 555 LKEMSHLETE--AEARATREAKYERLALDLFSECSNSEARAF-----ALLVRRNRC 605
 DB LOELSKVNEFSEVEBELSRCK--QFADLDQDRSSSELEIILNRYDNBL--EEGS 284
 229
 606 WSKTCLHATEADAKAFADGVQAFELTRV-----WQDMAAGTPIRLGAF 654
 DB GNDLRLKLAIKYRKEFEVAQPCOOLLASRWYDEFGWRRRHVAWKVTCFVGL--F 342
 285
 655 LCFALVYNTLIFSEBAPRTGLELDLQDLSLDTESPLVYGSVEBELVEAPRAQGRG 714
 DB LCFALVYNTLIFSEBAPRTGLELDLQDLSLDTESPLVYGSVEBELVEAPRAQGRG 714
 343 PVFSVCY-----LIAPSPV--GL----- 359
 745 PRAVELTRWRKFGAPVTFELGNVVPAPFLFLFTYVL-----VDRPPQGPS 765
 DB PRAVELTRWRKFGAPVTFELGNVVPAPFLFLFTYVL-----VDRPPQGPS 765
 360 -----FIKRFIKFICHTASVLTFL--LLASQHIDRSLNQGPP--PT 402
 766 GBEVTLVYFVFLVLEIRQ--GEFTDETHLVKKFTLVYGDNNKCDMAIFLTVGV 822
 DB GBEVTLVYFVFLVLEIRQ--GEFTDETHLVKKFTLVYGDNNKCDMAIFLTVGV 822
 403 IYEMWILPWLGVFNGEIKQMDGLQD-----YIHDWNLMDPVNNSLYLATI 451
 823 TCRMLP--SAFE-----AGRTVLDMPVFTLRLHFAHKOLGPKIIV 866
 DB TCRMLP--SAFE-----AGRTVLDMPVFTLRLHFAHKOLGPKIIV 866
 452 SKIIVAFVKYSALNPRESWDMHPVLVAELFALIANISSLRISLFTANSHLGPQLSL 511
 867 ERMKDVFFFLFELSVLVAY-----GVTTOAL-LPHDGRLEWIFRYVL 910
 DB ERMKDVFFFLFELSVLVAY-----GVTTOAL-LPHDGRLEWIFRYVL 910
 512 GMDLDILKFLTYCLVLAFLANGNLQLYFYEBETGSCCKRGKONARSTLF-ETL 570
 911 YRPVLIQFQPLDEIDEARVNCSTHPLLEDSPCPSLYANWLVLLVTLVTLVTL 970
 DB YRPVLIQFQPLDEIDEARVNCSTHPLLEDSPCPSLYANWLVLLVTLVTLVTL 970
 571 OSLFWSIFGLIN-----LYVNVKQHEFTFEVGTATGTYNVISLVVL 614
 971 NMLLIAMPSYTOVVOGNATMFKFORVNLVIEYHERPALP--PELL----- 1017
 DB NMLLIAMPSYTOVVOGNATMFKFORVNLVIEYHERPALP--PELL----- 1017
 615 LMLLIAMNNSTYQLADHADIEKFKRTKLMSTYFEEGGTLPLPEFNIVSPKSLWYLW 674
 1018 --SHL-SLTLR-----VFKEAEH-KREHLERDLPPLDQKV-----TWETVO 1058
 DB --SHL-SLTLR-----VFKEAEH-KREHLERDLPPLDQKV-----TWETVO 1058
 675 IYTHLCKKMRKRKESFGITGRADNLRHHQYGVMMNLVRYVAAMIRAKTEEGTL 734
 1059 KENF-----LSQKEK-----RRDSEG----- 1075
 DB KENF-----LSQKEK-----RRDSEG----- 1075
 735 EENFKELKODISSFREVELGLRGSLTVOSNOGTKESSNSADSEKSDNEGSKDKK 794
 1076 -----EVLAKTAHVRVDPIA--KYLQGLREGE 1099
 DB NSSLPLTLTLIHRSAIAIAERHTTISNGSALVQBPPEKQKRVNVTIRHGLFHRSS 854
 795
 1100 KRIKLESQINCVSVSVADVLAQGGPRSSQ-----HCGEGSQLVAAADH 1146
 DB KRIKLESQINCVSVSVADVLAQGGPRSSQ-----HCGEGSQLVAAADH 1146
 855 KQHAAEQUNANQFVSSEGAQAQAGPLERSIQLSRTLASKGDLNITGLSQCLVVDH 914
 1147 R 1147
 DB 915 R 915
 RESULT 13
 TRP4 HUMAN STANDARD; PRT; 977 AA.
 AC Q9UBN4; Q15721; Q9UB10; Q9UB1; Q9UB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Short transient receptor potential channel 4 (TRPC4) (trp-related
 protein 4) (htrp-4) (htrp4).
 DE TRPC4.
 GN

OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_Taxid=9606;
 RN
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Kidney;
 RX MEDLINE=2049875; PubMed=11042129;
 RA McKay R.R., Szymczek-Seay C.L., Lleyremont J.-P., Bird G.S., Zitt C.,
 RT Juengling E., Luckhoff A., Putney J.W. Jr.;
 RT "Cloning and expression of the human transient receptor potential 4
 TRP4 gene: localization and functional expression of human TRP4 and
 RL TRP4".
 RL Biochem. J. 351:735-746(2000).
 RN
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA, BETA, DELTA AND GAMMA).
 RC TISSUE=Embryonic Kidney;
 RX MEDLINE=2109836; PubMed=1163362;
 RA Mery L., Magnino F., Schmidt K., Krause K.-H., Dufour J.-F.,
 RT "Alternative splice variants of htrp4 differentially interact with the
 RT C-terminal portion of the inositol 1,4,5-trisphosphate receptors".
 RL FEBS Lett. 487:377-383(2001).
 RN
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=21671347; PubMed=11713258;
 RA Schaefer M., Plant T.D., Stresow N., Albrecht N., Schultz G.,
 RT "Functional differences between TRPC4 splice variants".
 RL J. Biol. Chem. 277:3752-3759(2002).
 RN
 RP SEQUENCE OF 514-633 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96234226; PubMed=8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RT Birbaumer L.;
 RT "trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry".
 RL Cell 85:661-671(1996).
 CC
 CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
 CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
 CC -1- SUBUNIT: Isoform alpha but not isoform beta associates with NHERF
 CC inositol-1,4,5-trisphosphate receptor (trpr). Interacts with NHERF
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=Alpha;
 CC IsoId=Q9UBN4-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9UBN4-2; Sequence=VSP_006566;
 CC Name=Delta;
 CC IsoId=Q9UBN4-3; Sequence=VSP_006566;
 CC Name=Gamma;
 CC IsoId=Q9UBN4-4; Sequence=VSP_006567, VSP_006569;
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PLACENTA. EXPRESSED AT
 CC LOWER LEVELS IN HEART, PANCREAS, KIDNEY AND BRAIN. ISOFORM ALPHA
 CC WAS FOUND TO BE THE PREDOMINANT ISOFORM. ISOFORM BETA WAS NOT
 CC FOUND IN PANCREAS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ANK repeats.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL; AF063822; AAF22927.1; -
DR EMBL; AF063823; AAF22928.1; -
DR EMBL; AF063824; AAF22929.1; -
DR EMBL; AF063825; AAF22930.1; -
DR EMBL; AF175406; AAD51736.1; -
DR EMBL; AF421358; AAL24549.1; -
DR EMBL; AF421359; AAL24550.1; -
DR EMBL; U40983; AAC50630.1; -
DR GeneW; HGNC:12336; TRPCA.
DR MIM; 603651; -
DR GO; GO:0015279; P:store-operated calcium channel activity; TAS.
DR GO; GO:0006816; P:calcium ion transport; TAS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrypL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR002153; Trans receptor.
DR InterPro; IPR004729; Tryp Ca channel.
DR InterPro; IPR005460; TRP channel4.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR PRINTS; PR01645; TRPCHANNEL4.
DR SMART; SM00248; ANK; 2.
DR TIGRfam; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_RBP_REGION; 1.
DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
KV ANK repeat; Repeat; Alternative splicing.
KV DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 330 350 POTENTIAL.
FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 363 383 POTENTIAL.
FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 437 457 POTENTIAL.
FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 512 532 POTENTIAL.
FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 600 620 POTENTIAL.
FT DOMAIN 621 977 CYTOPLASMIC (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 141 170 POLY-LEU.
FT DOMAIN 377 382 ANK 2.
FT DOMAIN 615 977 BINDS TO ITPR1, ITPR2 AND ITPR3.
FT SITE 972 974 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN (BY SIMILARITY).
FT VARSPLIC 629 693 Missing (in isoform Gamma).
FT VARSPLIC 730 870 /FTId=VSP_006567.
FT VARSPLIC 785 868 Missing (in isoform Delta).
FT VARSPLIC 785 868 Missing (in isoform Beta and isoform Gamma).
SQ SEQUENCE 977 AA; 112100 MM; 77E4D27C374D660E CRC64;
Query Match 3.6%; Score 219.5; DB 1; Length 977;
Best Local Similarity 19.9%; Pred. No. 8,6e-07;
Matches 156; Conservative 104; Mismatches 235; Indels 289; Gaps 34;
QY 555 LKNSHLETE--AEARATREAKYERLALDLFSECYNSSEARAF-----ALVRRNRRC 605
DB 227 LQELSKVENEPKSEYBELSRQCK--QPAKDLDDQRRSSSELEIILNYRDNLSLI--EQGS 282
QY 606 WSKTICHLATEADAKAFPAHDGVAFLTRIV-----WGDMAAGPIRLLGAF 654
DB 283 GNDLARLKLAIKYRKEFEVAQPCOOLASRWYDEFPGRRRHWAVKWTCTFIIGLL--F 340
QY 655 LCFALVYTNLITFSEAPLRTGLDLDLDTESKPLYGQSVBELVEAPRAQSGRG 714
DB 341 PVFSVCY-----LIARKSPJ-GL-----VDFRPPPGQPS 765
QY 715 PRAVELLTRRRKKGAPVTVFLGNVVMYFAFLFLFTYVLL-----VDFRPPPGQPS 765

DB 358 -----FIRKPIKFICHTASYLTLFL-----LLLASQIHDSRLNRQGP--PT 400
QY 766 GPEVTVYFWVFLTVLEIRQ---GFETDEDHLVKKFLUYGDNNKCDMAVFIPIYGV 822
DB 401 IVEWMILFWVLGFTIGELIKOMDGLD-----YHDMNMLDPVNSLYLTI 449
QY 823 TCRMLP--SAFE-----ACRTVLAMDFWVFTLRLIHFAIHKQGPRIIV 866
DB 450 SLKIVAFPKYSALNRESMDMMHPTLVAEALFAININISSRLISLFTANSHLGLOSL 509
QY 867 ERMKQDVFFFLFELSVLVAI-----GYTQAL-LHPDGRLEWIFRVL 910
DB 510 GRMLDILKFLFIYCLVILAFANGINQLFYEEETKGLCKGIRCEKONAFSTLF-BTL 568
QY 911 YRPVQIRGQIPLDEIDARNCSTHPLLEDSPCBCLYANWLVILLVFLVTVNVL 970
DB 569 QSLFWSITGLIN-----LYTVNKAQHETFEFGATMGITVNVISLVVL 612
QY 971 NMLLIAMFSYFOVQGNATWFMKFORYNLIVEYHERPALAP-PEILL----- 1017
DB 613 LNMLIAMNNNSYQLADADLEMKFARFKLMSYFEEGTLPTFPNVIPSPKSLWYLLKM 672
QY 1018 --SHL-SITLRR-----VKKKEAEH-KREHLERDLPDPLDQKV-----TWETVQ 1058
DB 673 IWTHLCKKMKRKRKESFGTIGRRADNLRHRRHQEVVRNLVRYVAMIRDAKTEGTL 732
QY 1059 KENF-----LSKMEK-----RRDSG----- 1075
DB 733 EENFELKODISSPREFVLGLRSGKSTIOSANASKSSNSADSDESGSKDKKK 792
QY 1076 -----EVLKRTARVDYFIKYLQ-GLREQEK 1100
DB 793 NPSLEDTLTHPSAATASERHNINSALVQEPREPKRKNNFYDINKFGLFHRS 852
QY 1101 RIKLIESQINCSVLVSSVADVLA--QGSGP--RSSQHCSE-----SOLVA 1143
DB 853 KONAEOQANQ-----IFSVSEVARQQAAGLERNIQLESGLASRGDISIFGLSEQCVL 908
QY 1144 ADHR 1147
DB 909 VDRH 912
RESULT 14
TRP4_MOUSE STANDARD; PRT; 974 AA.
ID TRP4_MOUSE
AC Q9Q0Q5; Q62350; Q9Q0Q9; Q9Q2C0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short transient receptor potential channel 4 (TrpC4) (Receptor-
activated cation channel TRP4) (Capacitance calcium entry channel
Trp4).
DE GN TRPCA OR TRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC Tissue=Brain;
RT Zhu X., Boulay G., Jiang M., Birbaumer L.;
RT "Trp4 is involved in capacitative calcium entry in murine cells.";
RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RA Qian F., Phillips L.H.;
RL Submitted (Mar-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC Tissue=Brain;
RX MEDLINE=98171352; PubMed=9512398;


```

Oy 911 YRPVIGIQGPPLBIDARVNCSTHPLLEDSPSCPSLYANWVILLVTLVLTNVLL 970
Db 569 QSLFMSIGLIN-----LYTNVNAQHHEFFEFVATFETYNVLSLVL 612
Oy 971 NMLLIAMSTYFQVQGNATWPKFQRYNLIVEYHERPALAP-PTLL----- 1017
Db 613 LNMILIAMNNNSYQIADADIDEMKFAFKLWMSYFEEGGLTFPPNVVSPSKLWYLVKW 672
Oy 1018 --SHL-STLLRR-----VFKKEAHEKREHLERDLPDPLDOKVVTWTVOK--ENFLS 1064
Db 673 IWLHLCKKMRKRPESFGTIGRADNLRHHQ-----YQEWRLNVKRYVA 719
Oy 1065 KMEKRRRPSG---EVLAKTARV-DFAKYLIGIGREOEKRIKLESQINTCSVLVSSVA 1120
Db 720 AMIREAKTEBGLTENENVELKODISSFRFEVLGLRGSKL-----STQSANMASSADS 773
Oy 1121 DVLAGGGG-----PRSSOHGGE-----GSQLVAD 1145
Db 774 DEKQSENGKDKRKNLSLFDLTLIHPRSAIASERHNLNSGSLVVOE 823

RESULT 15
TRP4_RAT STANDARD: PRT: 977 AA.
AC 035119; Q9EQ74; Q9EQ75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short transient receptor potential channel 4 (Trpc4) (Trp4)
DE (Capacitative calcium entry channel 1) (CCE1).
CN TRPC4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=Wistar Imamichi; TISSUE=Brain;
RX MEDLINE=97189270; PubMed=9037541;
RA Funayama M., Goto K., Kondo H.;
RT "Cloning and expression localization of cDNA for rat homolog of TRP
RT protein, a possible store-operated calcium (Ca2+) channel.";
RL Brain Res. Mol. Brain Res. 43:259-266(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=20545496; PubMed=10980202;
RA Tang Y., Tang J., Chen Z., Trost C., Flockertzi V., Li M., Ramesh V.,
RA Zhu W.X.;
RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ
RT domain-containing protein, NHERF.";
RL J. Biol. Chem. 275:37559-37564(2000).
CC -1- FUNCTION: THOUGHT TO FORM NON-SELECTIVE A RECEPTOR-ACTIVATED
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES WITH
CC INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERF
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=035119-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=035119-2; Sequence=VSP 006571;
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB008889; BAA2359.1; -
DR EMBL; AF288407; AAC21809.1; -
DR EMBL; AF288408; AAC21810.1; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cal_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR002153; Trans_receptor.
DR InterPro; IPR004729; Trp_CaChannel.
DR InterPro; IPR005460; TRPChannel4.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion_trans.1.
DR PRINTS; PRO1097; TRNSRCEPTRP.
DR PRINTS; PRO1645; TRPCHANNEL4.
DR SMART; SMO0248; ANK; 2.
DR TIGRfam; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 329
FT TRANSMEM 330 350
FT DOMAIN 351 362
FT TRANSMEM 363 383
FT DOMAIN 384 436
FT TRANSMEM 437 457
FT DOMAIN 458 469
FT TRANSMEM 470 490
FT DOMAIN 491 511
FT TRANSMEM 512 532
FT DOMAIN 533 599
FT TRANSMEM 600 620
FT DOMAIN 621 974
FT REPEAT 69 98
FT REPEAT 141 170
FT DOMAIN 141 170
FT SITE 975 977
FT VASPLIC 784 867
FT CONFLICT 11 11
FT CONFLICT 72 76
FT CONFLICT 121 135
FT CONFLICT 204 204
FT CONFLICT 385 411
FT CONFLICT 681 681
FT CONFLICT 705 705
FT CONFLICT 728 728
FT CONFLICT 807 807
FT CONFLICT 873 873
FT CONFLICT 888 888
FT CONFLICT 922 977
SO SEQUENCE 977 AA; 111847 MW; 6F86DA95261E0EDC CRC64;
Query Match 3.5%; Score 216; DB 1; Length 977;
Best Local Similarity 20.2%; Pred. No. 1.5e-06;
Matches 130; Conservative 94; Mismatches 208; Indels 210; Gaps 27;
Oy 555 LKMSHETE--AEAAATREAKTERLALDFSECVNSSEARAF-----ALVRRNC 605
Db 227 LOELSKVENEFKSEYELSRQCK--QFADLDOTRSSRELITILNYRDNDSLI--EES 282

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: September 10, 2003, 09:41:20 ; Search time 33 Seconds
(without alignments)
5151.151 Million cell updates/sec

Title: US-09-834-792C-4
Perfect score: 6091
Sequence: 1 MDVQGRPPSPGDAEDRRE.....HRGIDGWEQPGAGQPSPTD 1165

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues
Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubppaa/US10C_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6075.5	99.7	1164	9	US-09-834-792-5
2	6073	99.7	1165	14	US-10-026-188-8
3	5068.5	83.2	1158	9	US-09-834-792-2
4	5068.5	83.2	1158	14	US-10-026-188-5
5	4988.5	81.9	1165	14	US-10-026-188-2
6	2430.5	39.9	1214	12	US-10-142-649-2
7	2335	38.3	1083	10	US-09-789-841C-2
8	2041	33.5	1503	12	US-10-153-244-104
9	2041	33.5	1503	14	US-10-210-152-21
10	1578	25.9	1104	12	US-10-171-319-8
11	1578	25.9	1104	14	US-09-759-143-778
12	1562.5	25.7	1095	9	US-09-780-669-778
13	1562.5	25.7	1095	9	US-09-822-827-778
14	1562.5	25.7	1095	9	US-09-822-827-778
15	1562.5	25.7	1095	10	US-09-895-793-778

16	1562.5	25.7	1095	10	US-09-895-814-778	Sequence 778, App
17	1562.5	25.7	1095	12	US-10-144-678A-778	Sequence 778, App
18	1562.5	25.7	1095	14	US-10-012-896-778	Sequence 778, App
19	1562.5	25.7	1095	15	US-10-205-823-421	Sequence 421, App
20	1554.5	25.5	1095	12	US-10-171-319-11	Sequence 11, App1
21	1554.5	25.5	1095	9	US-09-759-143-780	Sequence 780, App
22	1554.5	25.5	1095	9	US-09-780-669-780	Sequence 780, App
23	1554.5	25.5	1095	9	US-09-822-827-780	Sequence 780, App
24	1554.5	25.5	1095	10	US-09-895-793-780	Sequence 780, App
25	1554.5	25.5	1095	10	US-09-895-814-780	Sequence 780, App
26	1554.5	25.5	1095	12	US-10-144-678A-780	Sequence 780, App
27	1554.5	25.5	1095	14	US-10-012-896-780	Sequence 780, App
28	1305.5	21.4	1566	12	US-10-210-152-6	Sequence 6, App1
29	1300.5	21.4	1544	12	US-10-210-152-2	Sequence 2, App1
30	1300.5	21.4	1554	12	US-10-210-152-2	Sequence 2, App1
31	1296.5	21.3	1556	12	US-10-210-152-9	Sequence 9, App1
32	1296.5	21.3	1566	12	US-10-210-152-4	Sequence 4, App1
33	1293	21.2	1579	12	US-10-210-152-10	Sequence 10, App1
34	1228.5	20.2	1533	9	US-09-828-466-7	Sequence 7, App1
35	1228.5	20.2	1533	10	US-09-946-175-1	Sequence 1, App1
36	1228.5	20.2	1533	10	US-09-989-820-259	Sequence 259, App
37	1228.5	20.2	1533	12	US-10-153-244-260	Sequence 260, App
38	1228.5	20.2	1533	12	US-10-210-152-11	Sequence 11, App1
39	1228.5	20.2	1533	15	US-10-281-644-9	Sequence 9, App1
40	1217	20.0	1393	15	US-10-058-513-2	Sequence 2, App1
41	1208.5	19.8	1863	10	US-09-832-292-29	Sequence 29, App1
42	1189.5	19.5	1864	10	US-09-832-292-27	Sequence 27, App1
43	1184	19.4	1970	12	US-10-153-244-4	Sequence 4, App1
44	1183.5	19.4	1864	12	US-10-153-244-6	Sequence 6, App1
45	1180.5	19.4	1939	12	US-10-153-244-6	Sequence 6, App1

ALIGNMENTS

RESULT 1
US-09-834-792-5
Sequence 5, Application US/09834792
Parent No. US20020037515A1
GENERAL INFORMATION:
APPLICANT: Mount Sinai School of Medicine of NYU
TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
FILE REFERENCE: AP32911 070165 0589
CURRENT APPLICATION NUMBER: US/09/834, 792
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,491
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1164
TYPE: PRT
ORGANISM: Human
US-09-834-792-5

Query Match	99.7%	Score 6075.5;	DB 9;	Length 1164;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1164;	Conservative	0;	Mismatches	0;
			Indels	1;
			Gaps	1;
Qy	1	MDVQGRPPSPGDAEDRREGLHGRGVNFGSGKKRKFVPSVGLPDLAEM	60	
Db	1	MDVQGRPPSPGDAEDRREGLHGRGVNFGSGKKRKFVPSVGLPDLAEM	60	
Qy	61	HLPAFNLVSLVGEQPFPAKSWLRLKGLVLAQSTGAWILTSALRYGLAHVGOAV	120	
Db	61	HLPAFNLVSLVGEQPFPAKSWLRLKGLVLAQSTGAWILTSALRYGLAHVGOAV	120	
Qy	121	RDSHSLASTSKRVAVVAVGASLGRVLRRLLEAEQDFPVHYPPDDGSGGCLSDSNL	180	
Db	121	RDSHSLASTSKRVAVVAVGASLGRVLRRLLEAEQDFPVHYPPDDGSGGCLSDSNL	180	
Qy	181	SHFLVPPGPKKDDGLTELRLRLKRIISQRAVGYGTGSIETPVCLLVNGDPNTLERI	240	

Dd	181	SHFLVBERGPPGKGDGLTELRLRLEKHSI80RAGYGGGSI8I8IVLCLLVANGDPTNLTJ8RI	240
Qy	241	SRAVEQAAPWILIVSGGSIADIVLAALVNOPHILVPRVAEKOPFKKEFP8KHSWEDIYWT	300
Dd	241	SRAVEQAAPWILIVSGGSIADIVLAALVNOPHILVPRVAEKOPFKKEFP8KHSWEDIYWT	300
Qy	301	KLONITSHOHLITVYDEOGGSEELDVIIKALVKAOKHSIO8QDYLDELKTLAVADR	360
Dd	301	KLONITSHOHLITVYDEOGGSEELDVIIKALVKAOKHSIO8QDYLDELKTLAVADR	360
Qy	361	VDIAKSEIF8NDVEMKSCDLE8VWMDALVSNKPEFVRLFVNDGADVADFLTLYGRLOELYR	420
Dd	361	VDIAKSEIF8NDVEMKSCDLE8VWMDALVSNKPEFVRLFVNDGADVADFLTLYGRLOELYR	420
Qy	421	SV8K8SLLPDLLORQ8E8ARLTLA8LGTOQ8AREP8AG8AP8I8H8V8VL8D8FOD8AC8RG	480
Dd	421	SV8K8SLLPDLLORQ8E8ARLTLA8LGTOQ8AREP8AG8AP8I8H8V8VL8D8FOD8AC8RG	480
Qy	481	FYOD8RPGD8R8RA8E8K8P8AK8PT8G8K8ML8D8N8K88NP8RDL8FL8M8VL8ON8H8MAT8Y8FW8M	540
Dd	481	FYOD8RPGD8R8RA8E8K8P8AK8PT8G8K8ML8D8N8K88NP8RDL8FL8M8VL8ON8H8MAT8Y8FW8M	540
Qy	541	GO8G8VA8A8L8ACK8I8K88SH8L8TE8EA8AR8ATE8A8Y8ER8AL8DL8F88C8Y8NS88AR8AF8ALLY	600
Dd	541	GO8G8VA8A8L8ACK8I8K88SH8L8TE8EA8AR8ATE8A8Y8ER8AL8DL8F88C8Y8NS88AR8AF8ALLY	600
Qy	601	R8NR8C8MS8KTT8CH8LT8E8AD8AK8AF8A8HD8G8QA8FL8TRI8M8GD8MA8G8PI8RL88A8F8IC8F8ALY	660
Dd	601	R8NR8C8MS8KTT8CH8LT8E8AD8AK8AF8A8HD8G8QA8FL8TRI8M8GD8MA8G8PI8RL88A8F8IC8F8ALY	660
Qy	661	YTNLT8F88E8A8RL8TG8L8D8LO8DL88D8L8TE8K88P8LY8G8I888V88E8L8VE8P8RA88G8R8P8AV8L	720
Dd	661	YTNLT8F88E8A8RL8TG8L8D8LO8DL88D8L8TE8K88P8LY8G8I888V88E8L8VE8P8RA88G8R8P8AV8L	720
Qy	721	L8TR8MK8K8F8M8CA8PT8VL8GN8V8M8F8AL8FL8TY8VL8D8FR8PP88G8888E8V8TL8FW8FT8VL	780
Dd	721	L8TR8MK8K8F8M8CA8PT8VL8GN8V8M8F8AL8FL8TY8VL8D8FR8PP88G8888E8V8TL8FW8FT8VL	780
Qy	781	BE8IR8G8F8P8D8ED8TH8Y8K8K8FT8LY8G8DN8M8K8D8M8VA8FL8F8V8T8CR8ML8PS8A8F8AG8RT8VL8M	840
Dd	781	BE8IR8G8F8P8D8ED8TH8Y8K8K8FT8LY8G8DN8M8K8D8M8VA8FL8F8V8T8CR8ML8PS8A8F8AG8RT8VL8M	840
Qy	841	DM8V8T8L8RL8IH8F8A8HK88G8PK8I8Y8ER8M8K8OV8FF8L8FL88V8L8VA8Y8GTT8Q8ALL8PH8G	900
Dd	841	DM8V8T8L8RL8IH8F8A8HK88G8PK8I8Y8ER8M8K8OV8FF8L8FL88V8L8VA8Y8GTT8Q8ALL8PH8G	900
Qy	901	PL8EM8I8FR8VL8Y8P8Y8LO8IF8GO8I8PL8DE8ID8AR8V8NC88TP8LL8ED88P88C8PS8I8Y8AN8VL8T8LL8V	960
Dd	901	PL8EM8I8FR8VL8Y8P8Y8LO8IF8GO8I8PL8DE8ID8AR8V8NC88TP8LL8ED88P88C8PS8I8Y8AN8VL8T8LL8V	960
Qy	961	TE8LL8V8TN8VL8M8N8LL8M88SY8T8FO8V8G8N8AT8M8FK8FOR8YN8LY8E8H8RR8PAL8AP8F8ILL8SH8L	1020
Dd	961	TE8LL8V8TN8VL8M8N8LL8M88SY8T8FO8V8G8N8AT8M8FK8FOR8YN8LY8E8H8RR8PAL8AP8F8ILL8SH8L	1020
Qy	1021	SL8TR8V8F8PK8E8A8H8K88E8H8ER8DL8PD8LD8Q8V8W8E8V8Q8EN8F8LS8K8E8K8RR8D888E88VL8RK	1080
Dd	1021	SL8TR8V8F8PK8E8A8H8K88E8H8ER8DL8PD8LD8Q8V8W8E8V8Q8EN8F8LS8K8E8K8RR8D888E88VL8RK	1080
Qy	1081	TA8R8V8D8F8I8AK8YL8G8L88E88K8I8K8L888Q8I8NC88VL88SV8AD8VL8A8G8G88P88888Q888G8888Q	1140
Dd	1081	TA8R8V8D8F8I8AK8YL8G8L88E88K8I8K8L888Q8I8NC88VL88SV8AD8VL8A8G8G88P88888Q88888Q88888Q	1140
Qy	1141	LV8A8D8R8G8G8I8DG8E8Q8P8AG8Q8P88D8T	1164
Dd	1141	LV8A8D8R8G8G8I8DG8E8Q8P8AG8Q8P88D8T	1164

RESULT 2
US-10-026-188-8
; Sequence 8, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:

```

1  APPLICANT: Zuker, Charles S.
2  APPLICANT: Zhang, Yifeng
3  APPLICANT: The Regents of the University of California
4  TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
5  TITLE OF INVENTION: Ion Channel
6  FILE REFERENCE: 02307E-114910US
7  CURRENT APPLICATION NUMBER: US/10/026,188
8  CURRENT FILING DATE: 2001-12-21
9  PRIOR APPLICATION NUMBER: US 60/259,379
10 PRIOR FILING DATE: 2000-12-29
11 NUMBER OF SEQ ID NOS: 8
12 SOFTWARE: FastSeq for Windows Version 3.0
13 SEQ ID NO 8
14 LENGTH: 1165
15 TYPE: PRT
16 ORGANISM: Homo sapiens
17 FEATURE:
18 OTHER INFORMATION: human lrrpc6
19 US-10-026-188-8

```

Query Match	99.7%: Score 6073; DB 14; Length 1165;
Best Local Similarity	99.7%: Pred. No. 0;
Matches 1162; Conservative	1; Mismatches 2; Indels 0; Gaps 0;
Qy 1	MQDVGGPPGSPGGAEDRFEIGLHGRGEVNFSGSGKKRGKPFVRVSGVAPSVLFDLLLAEW 60
Db 1	MQDVGGPPGSPGGAEDRRELGLHGRGEVNFSGSGKKRGKPFVRVSGVAPSVLFDLLLAEW 60
Qy 61	HLPAENVLSVGEEOFPAPMKSWLRLVLRKGLVKAOSTGAWILTSALRVGLAHVGOAV 120
Db 61	HLPAENVLSVGEEOFPAPMKSWLRLVLRKGLVKAOSTGAWILTSALRVGLAHVGOAV 120
Qy 121	RDHSLASTSTVRRVAVANGMASLGRVLRHRIIEEAQEDPPHYPPEDDGSOSPLCSLSNL 180
Db 121	RDHSLASTSTKVRVAVANGMASLGRVLRHRIIEEAQEDPPHYPPEDDGSOSPLCSLSNL 180
Qy 181	SHFLIVEGPPGKDGGLTELRLRLKHSIQRAGVGGTSEIPLCLLVNGDPITLIERI 240
Db 181	SHFLIVEGPPGKGGGLTELRLRLKHSISEPAGVGGTSEIPLCLLVNGDPITLIERI 240
Qy 241	SRAVEQAPMWILVSGGIDAVLVAALVNPQHLVPRVAKQPFKEFSPKSHSWEDEVMT 300
Db 241	SRAVEQAPMWILVSGGIDAVLVAALVNPQHLVPRVAKQPFKEFSPKSHSWEDEVMT 300
Qy 301	KLLQNTITSHQHLITVYDPEOEGSEBELTVILKALVYACKSHSQEPODYLDLKLAVAMDR 360
Db 301	KLLQNTITSHQHLITVYDPEOEGSEBELTVILKALVYACKSHSQEPODYLDLKLAVAMDR 360
Qy 361	VDIAKSEIFNGDVEWKSCDLEBVMYDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
Db 361	VDIAKSEIFNGDVEWKSCDLEBVMYDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
Qy 421	SYSRSKSLFDLLQRQOEEARLTLAIGLGTQOAREPAPGPAFSLHVSIVLXQFLDADCRG 480
Db 421	SYSRSKSLFDLLQRQOEEARLTLAIGLGTQOAREPAPGPAFSLHVSIVLXQFLDADCRG 480
Qy 481	FVQDPRPGDRRRAEKGPAKPTGQKMLDLNOKSENPMRDLFLMAVLQNRHEMATYFWAM 540
Db 481	FVQDPRPGDRRRAEKGPAKPTGQKMLDLNOKSENPMRDLFLMAVLQNRHEMATYFWAM 540
Qy 541	GOEGVAALAAKCIKEMSHLETEEAARATEAERYERIALDLFSECYSNSBARAFALLV 600
Db 541	GOEGVAALAAKCIKEMSHLETEEAARATEAERYERIALDLFSECYSNSBARAFALLV 600
Qy 601	RNRRCMSKTTCLHLATEADAKAFPAHVGQAFLTRIIMGDMAAGPIRLILGAFICFALV 660
Db 601	RNRRCMSKTTCLHLATEADAKAFPAHVGQAFLTRIIMGDMAAGPIRLILGAFICFALV 660
Qy 661	YTNLITTFSEEARLTGLEDLQDLSDLTEKSPLYGLQSFVEELVLEAPRAQSGRGPAVFL 720
Db 661	YTNLITTFSEEARLTGLEDLQDLSDLTEKSPLYGLQSFVEELVLEAPRAQSGRGPAVFL 720
Qy 721	LTRRRKFKGAPVTVEFGVNVMTFAFLFLFTYVLVLDFFRRPGGSGPEVTLYLFWVETVLV 780


```

Db      721 LTRMKKEGAPVTVFLGNVMTFAFLFTTYLLVDPRPPQSGPGEVTLTFWFTVL 780
Qy      781 BEIRGPFTEDETHLVKFTLVYGDNNKCDMAVAFLEIVGTCMLPSAFEAGRTVLAM 840
Db      781 BEIRGPFTEDETHLVKFTLVYGDNNKCDMAVAFLEIVGTCMLPSAFEAGRTVLAM 840
Qy      841 DEMVTTLRLLIHFAIHKQIGPKIIVERMKDVPFFLFSLVWLVAVGTTQALLHPDG 900
Db      841 DEMVTTLRLLIHFAIHKQIGPKIIVERMKDVPFFLFSLVWLVAVGTTQALLHPDG 900
Qy      901 RLEWTFRRVLRVYQIQIGQIPLEIDEARVNCSTHPLLEDSPCSLXANMVLITLLV 960
Db      901 RLEWTFRRVLRVYQIQIGQIPLEIDEARVNCSTHPLLEDSPCSLXANMVLITLLV 960
Qy      961 TELLVTVNLMLNLLIAMSSTFYQVQGNATMFKFORVNLIVEYHERPALAPFILLSHL 1020
Db      961 TELLVTVNLMLNLLIAMSSTFYQVQGNATMFKFORVNLIVEYHERPALAPFILLSHL 1020
Qy      1021 SILLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVQENFLSXMEKRRRDEGEVLRK 1080
Db      1021 SILLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVQENFLSXMEKRRRDEGEVLRK 1080
Qy      1081 TAHRRVDFIAKYIGLREDEKRIKLESQINVCYVSSVADYVLAQGGPRSSQHCGBSSQ 1140
Db      1081 TAHRRVDFIAKYIGLREDEKRIKLESQINVCYVSSVADYVLAQGGPRSSQHCGBSSQ 1140
Qy      1141 LVAADHGGIDGMEQPGAGQPPSDT 1165
Db      1141 LVAADHGGIDGMEQPGAGQPPSDT 1165

```

```

RESULT 3
US-09-834-792-2
; Sequence 2, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICATION: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; FILE REFERENCE: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; CURRENT APPLICATION NUMBER: US/09/834,792
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Murine TRP8
US-09-834-792-2

```

```

Query Match      83.2%; Score 5068.5; DB 9; Length 1158;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

```

```

Qy      1 MODVGGPRGSRGDEDRRELGLHRCGEVNFPGSGKKRKFVRVPSGVAPSVLFDLLALW 60
Db      1 MOTTSSCPGSPPTDEGMEPLLCRGEINFGSGKKRKFVPSVAPSVLFEILLTEW 60
Qy      61 HLPAPNLVSVLGEORPFAKMSMLRDVLKGLVKAOSTGAMILLTSALRVGLARHVGAV 120
Db      61 HLPAPNLVSVLGEORPFAKMSMLRDVLKGLVKAOSTGAMILLTSALRVGLARHVGAV 120
Qy      121 RDHSLASTSTKRVVAVAGMASIGRVLRRIIE--EAQEDPVHVREDGSGGPICLSDS 178
Db      121 RDHSLASTSTKRVVAVAGMASIGRVLRRIIE--EAQEDPVHVREDGSGGPICLSDS 178
Qy      179 NLSHFLLVPEPPGPKG-DGLTELRLRLKHTSEQAGVGGGSLIEPIVLCILVNGDPVTL 237
Db      179 NLSHFLLVPEPPGPKG-DGLTELRLRLKHTSEQAGVGGGSLIEPIVLCILVNGDPVTL 237
Qy      240 NLSHFLLVPEPPGPKG-DGLTELRLRLKHTSEQAGVGGGSLIEPIVLCILVNGDPVTL 240
Db      240 NLSHFLLVPEPPGPKG-DGLTELRLRLKHTSEQAGVGGGSLIEPIVLCILVNGDPVTL 240

```

```

Qy      238 ERISRAVEQAAPWLLIVSGGIAADVLAALVNQPHLVPKVAEQKPEKPSKHSWEDIV 297
Db      241 ERISRAVEQAAPWLLIVSGGIAADVLAALVNQPHLVPKVAEQKPEKPSKHSWEDIV 300
Qy      298 RMTKLONITSHOHLTYVDEEGSEELDVITLKAIVKACKSHSOEPOVLDLKLAVA 357
Db      301 HMTLLONIYAAHPHLLTYVDEEGSEELDVITLKAIVKACKSHSOEPOVLDLKLAVA 360
Qy      358 WDRVDIAKSEIFNCDVEMKSCDLEENWADALVSNKPEFVRLFVNGADVADPLTYGRLOE 417
Db      361 WDRVDIAKSEIFNCDVEMKSCDLEENWADALVSNKPEFVRLFVNGADVADPLTYGRLOE 420
Qy      418 LYRSVSRKSLIFDLQRKQEBARLTLAGLGTQARREPPAGPAPSLHEVSRVLKDFLODA 477
Db      421 LYHSVS PKSLIFELLQRKHEBGRLLTAGLGAQARRELPIDGAPSLHEVSRVLKDFLODA 480
Qy      478 CRGFYQDGRPEDRRRAEKPRPTGQKWLDDLNKSENPFRDLFLNAVLONREMATYF 537
Db      481 CRGFYQDGRPEDRRRAEKPRPTGQKWLDDLNKSENPFRDLFLNAVLONREMATYF 536
Qy      538 WAMQEGVAAALAAKILKEMSHLETEAABARTRAKYERLALDLFSECVSNEBARAFA 597
Db      537 WAMQEGVAAALAAKILKEMSHLETEAABARTRAKYERLALDLFSECVSNEBARAFA 596
Qy      598 LLYRRNRKWSKTCLHLATEADAKAFPAHGVQAFLTRIMWGDMAAGTPILRLGAFICP 657
Db      597 LLYRRNRKWSKTCLHLATEADAKAFPAHGVQAFLTRIMWGDMAAGTPILRLGAFICP 656
Qy      658 ALVYTNLITTSBEAPLRTGLEDDLDLSDTEKSPLYGLOSREVELYEAPAAQDGRPRA 717
Db      657 ALIYTNLITTSBEAPLRTGLEDDLDLSDTEKSPLYGLOSREVELYEAPAAQDGRPRA 716
Qy      718 VELLTRMRKFWGAPVTVFLGNVMTFAFLFTTYLLVDPRPPQSGPGEVTLTFWFTVL 777
Db      717 AFLTRMRKFWGAPVTVFLGNVMTFAFLFTTYLLVDPRPPQSGPGEVTLTFWFTVL 776
Qy      778 LVLEIRIQGFTEDETHLVKFTLVYGDNNKCDMAVAFLEIVGTCMLPSAFEAGRTV 837
Db      777 LVLEIRIQGFTEDETHLVKFTLVYGDNNKCDMAVAFLEIVGTCMLPSAFEAGRTV 836
Qy      838 LAMPFWFTLRLLIHFAIHKQIGPKIIVERMKDVPFFLFSLVWLVAVGTTQALLHP 897
Db      837 LAMPFWFTLRLLIHFAIHKQIGPKIIVERMKDVPFFLFSLVWLVAVGTTQALLHP 896
Qy      898 HDGRLEWIFRRVLRVYQIQIGQIPLEIDEARVNCSTHPLLEDSPCSLXANMVLITL 957
Db      897 HDGRLEWIFRRVLRVYQIQIGQIPLEIDEARVNCSTHPLLEDSPCSLXANMVLITL 956
Qy      958 LLVTFLLVTVNLMLNLLIAMSSTFYQVQGNATMFKFORVNLIVEYHERPALAPFILL 1017
Db      957 LLVTFLLVTVNLMLNLLIAMSSTFYQVQGNATMFKFORVNLIVEYHERPALAPFILL 1016
Qy      1018 SHLSLTLRVFKKEAHEKREHLERDLPDLDQKVVTWETVQENFLSXMEKRRRDEGEV 1077
Db      1017 SHLSLTLRVFKKEAHEKREHLERDLPDLDQKVVTWETVQENFLSXMEKRRRDEGEV 1076
Qy      1078 LRKTAHRVDFIAKYIGLREDEKRIKLESQINVCYVSSVADYVLAQGGPRSSQHCGBSSQ 1137
Db      1077 LRKTAHRVDFIAKYIGLREDEKRIKLESQINVCYVSSVADYVLAQGGPRSSQHCGBSSQ 1136
Qy      1138 GSQLVAAHGGIDGMEQPGAGQPPSDT 1165
Db      1137 GSQLVAAHGGIDGMEQPGAGQPPSDT 1158

```

```

RESULT 4
US-10-026-188-5
; Sequence 5, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California

```

```

; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence
; US-10-026-188-5

Query Match      83.2%; Score 5068.5; DB 14; Length 1158;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

QY 1 MODVGPSPGADADRRELGLHGEVNFSGSGKKRGKFRVPSGVAPSVLPDLLAEW 60
DB 1 MOTTSSCPSPPTEDGWEPIICRGEINFGSGGKKRGKFRVPSGVAPSVLPDLLAEW 60
QY 61 HLPAPNLVSLVGEOPFAMKSMRLDVLARKGLVKAOSTGAMILTSALHVGARHVGAV 120
DB 61 HLPAPNLVSLVGEOPFAMKSMRLDVLARKGLVKAOSTGAMILTSALHVGARHVGAV 120
QY 121 RDHSLASTSTKRVAVAVAGASLGRVLRRILE--EAQEDFPVHYPEDDGSOGPLCSLDS 178
DB 121 RDHSLASTSTKRVAVAVAGASLGRVLRRILE--EAQEDFPVHYPEDDGSOGPLCSLDS 180
QY 179 NLSHFLVPEPPGKG-DGLTELRLLEKHISEORAGYGTGSIIEIPVCLLVNGDPNTL 237
DB 181 NLSHFLVPEPPGKG-DGLTELRLLEKHISEORAGYGTGSIIEIPVCLLVNGDPNTL 240
QY 238 EHSISRAVEAPMILVSGSGADIVLAALVNOPHLLVPVAKOPFEPKPSKHFMSMEDIV 297
DB 241 EHSISRAVEAPMILVSGSGADIVLAALVNOPHLLVPVAKOPFEPKPSKHFMSMEDIV 300
QY 298 RWTKLQNTTSHOHLTVDFEPEGSEEDTVILKALVACKSHSQPODYLDELKLAVA 357
DB 301 HHTELLQNTAHPHLLTVDFEPEGSEEDTVILKALVACKSHSQPODYLDELKLAVA 360
QY 358 MDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLFYDNGADVAADFLTTGRLOE 417
DB 361 MDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLFYDNGADVAADFLTTGRLOE 420
QY 418 LVRSVSRKSLFDLLORKEEARLTLAGICTQAEPAPPAFSLHEVSRVLKDFLOPA 477
DB 421 LVHSVSPKSLFELLQRKHEBGLTLTAGAQAARSLPTGLPFSLHEVSRVLKDFLOPA 480
QY 478 CRGFYODGRCRRRAEKPAKPTGQKWLIDLNOKSEPMWDLFLMAVLQNRHEMATYF 537
DB 481 CRGFYODG---RRMERGPKRRPAQKPLPDLRSRSEDPMDLFLMAVLQNRHEMATYF 536
QY 538 WAMGEGVAAALAAKCIILKEMSHLETEAPARATREAKYERLALDLPSCYCSNSEARAPA 597
DB 537 WAMGREGVAAALAAKCIILKEMSHLEKEAEVARTREAKYEQIALDLFSECYCSNSEARAPA 596
QY 598 LVRRRRCMSKTTCHLATEADAKAFPAHDGVOAFLTRIWMGMAGTILRLGLFLCF 657
DB 597 LVRRRHMSRTTCHLATEADAKAFPAHDGVOAFLTKIWMGMAGTILRLGLFLCF 656
QY 658 ALVYTLITFSEBAPRTGLLEDLQDSDLTDEKSPYGLQSRVEELVEAPRAQDGRPA 717
DB 657 ALITYTLITFSEBAPRTGLLEDLQDSDLTDEKSPYGLQSRVEELVEAPRAQDGRPA 716
QY 718 VELLTRWRKFWGAPVTFLGNVVMYPAFLFLFTYVLLVDFRPPQSGSGEVTLYWVFT 777
DB 717 AFLTRWRKFWGAPVTFLGNVVMYPAFLFLFTYVLLVDFRPPQSGSGEVTLYWVFT 776

```

```

QY 778 LVLEIRQGFETDDETHLVKKFTLYVGNMNMCMVAFLFIYGVTCMLPSAFEGRTV 837
DB 777 LVLEIRQGFETDDETHLVKKFTLYVEDNMNMCMVAFLFIYGVTCMVPSEAGRTV 836
QY 838 LAMPWVFTLLIHFALHKLQGLKIIYVENMKDVFLEFLSWLVAAGVTTQALLHP 897
DB 837 LAIDFWFTLLIHFALHKLQGLKIIYVENMKDVFLEFLSWLVAAGVTTQALLHP 896
QY 898 HDGRLEWIFRRVLRPYQIFGOIPLDEIDBARVNCSTHPLLEDSPSCPSLANYMVL 957
DB 897 HDGRLEWIFRRVLRPYQIFGOIPLDEIDBARVNCSTHPLLEDSPSCPSLANYMVL 956
QY 958 LVLFELVTVNLVNLMLTAMESYTFQVVGNAFMFKFORNLIVEYHERPALAPFTLL 1017
DB 957 LVLFELVTVNLVNLMLTAMESYTFQVVGNAFMFKFORNLIVEYHERPALAPFTLL 1016
QY 1018 SHLSITLRRVRKGAHKKRHELRDLPPLDQKVVYTVTVQKENFLSKMKRRRSEEV 1077
DB 1017 SHLSITLRRVRKGAHKKRHELRDLPPLDQKVVYTVTVQKENFLSKMKRRRSEEV 1076
QY 1078 LRKTAHRVDLAKYIGLRBQEKRIKLESQINVCYVLSVADVLAQGGPRSSQHC 1137
DB 1077 LRKTAHRVDLAKYIGLRBQEKRIKLESQINVCYVLSVADVLAQGGPRSSQHC 1136
QY 1138 GSQLVADHRGIDGMEOPGAGOPPSDT 1165
DB 1137 RSQPASARD-----EYLESGLPSSDT 1158

RESULT 5
US-10-026-188-2
; Sequence 2, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat L-TRP taste predicted protein
; US-10-026-188-2

Query Match      81.9%; Score 4988.5; DB 14; Length 1165;
Best Local Similarity 82.6%; Pred. No. 0;
Matches 963; Conservative 76; Mismatches 116; Indels 11; Gaps 3;

QY 1 MODVGPSPGADADRRELGLHGEVNFSGSGKKRGKFRVPSGVAPSVLPDLLAEW 60
DB 9 MEMAOSCPSPPTEDGWEPIICRGEINFGSGGKKRGKFRVPSGVAPSVLPDLLAEW 68
QY 61 HLPAPNLVSLVGEOPFAMKSMRLDVLARKGLVKAOSTGAMILTSALHVGARHVGAV 120
DB 69 HLPAPNLVSLVGEOPFAMKSMRLDVLARKGLVKAOSTGAMILTSALHVGARHVGAV 128
QY 121 RDHSLASTSTKRVAVAVAGASLGRVLRRILEEAQEDFPVHYPEDDGSOGPLCSLDS 180
DB 123 RDHSLASTSTKRVAVAVAGASLGRVLRRILEEAQEDFPVHYPEDDGSOGPLCSLDS 188
QY 181 SHFLVPEPPGKG-DGLTELRLLEKHISEORAGYGTGSIIEIPVCLLVNGDPNTLER 239
DB 189 SHFLVPEPPGKG-DGLTELRLLEKHISEORAGYGTGSIIEIPVCLLVNGDPNTLER 248

```

QY	240	ISRAVEAOAPWILIVGSGGIADIVLAALVNOQPHLIVPKVAEXKQFKXEPSEKSHSMDIYRW	299
Db	249	MSRAVEOAPWILIVGSGGIADIVLAALVNOQPHLIVPQVTEKQFKREKFPSECSMEIYVM	308
QY	300	TKLONITSHOHLITVYDFEOEGSEELDVILKAVVKACKSHSOEPODYLDLKLAVAM	359
Db	309	TELLONIAHPHLITVYDFEOEGSEELDVILKAVVKACKSHSRADYLDLKLAVAM	368
QY	360	RVDIAKSEIFNGDVWKSCDLEEVDALVSKPEFVRLFDVNGADVADFTYGRLOEY	419
Db	369	RVDIAKSEIFNGDVWKSCDLEEVDALVSKNPFVRLFDVNGADMAEFTYGRLOOY	428
QY	420	RSVRSKSLFPDLQKOEABRLTLAAGLGTQOAREBPAGPAPSLHEVSVYLDPLQDAR	479
Db	429	HSVRSKSLFELLERKHEBGRLLTGLAQOQTRKLPVGLPAPSLHEVSVYLDPLHADR	488
QY	480	GFYODGRBQDRRAEKGPAREPTGQKWLIDLQKSEMPRDLFLMAVLQNRHEMATYEMA	539
Db	489	GFYODG----RMEKRGPPKRPAGQKWLPLSRKSEDPRLDLMAVVLQNRHEMATYEMA	544
QY	540	MGQSEVAAALAAACKILKEMSHLETEAARATREAKYERFLADLPSECSNSDEAPAFLL	599
Db	545	MGREVAAALAAACKIKEMSHLEKEAEVARTREAKYERFLADLPSECSNSDEAPAFLL	604
QY	600	VRRNCSGKTTCLHATEADAAFAFPHGVQOAFILRIMWGDMAAGPILRLILGALCFAL	659
Db	605	VRRNCSKRTTCLHATEADAAFAFPHDVQOAFILRIMWGDATGPILRLILGATCPAL	664
QY	660	VYTNLITSEEARPLRTGLDODLSDLPTEKSPLYGLOSRYVELTEAPRAQDGRGPVAF	719
Db	665	IYTNLITSESDAPQGMDELDQEPDSDLMKESFLCSHGQGLEKLTAPARAPDLDGPQAF	724
QY	720	LLTRRRKRWGAPVWYFLGNGVWVYKAPFLPTTVLLVDRPRPQSGSGPEVTLYFVWFTLV	779
Db	725	LLTRRRKRWGAPVWYFLGNGVWVYKAPFLPTTVLLVDRPRPQSGSGPEVTLYFVWFTLV	784
QY	780	LEEIRQGFTEBDTHLVKKFTLYVGDNNKCMQMAIFLEIVGTVGRMLPSAFAEAGRTVLA	839
Db	785	LEEIRQGFTEBDTHLVKKFTLYVEDNNKCMQMAIFLEIVGTVGRMPSVFAEAGRTVLA	844
QY	840	MDFWFTLRLIHIFAIHQOGPKIIVVERMKDVFPLFELSVMVLVAAGVTTQALLDHPD	899
Db	845	IDFWFTLRLIHIFAIHQOGPKIIVVERMKDVFPLFELSVMVLVAAGVTTQALLDHPD	904
QY	900	GRLEWIFRRVLVYRPLQIFGQIPLDEIDBARNGSTHPLLEDSPSCSLVIANMLVILLL	959
Db	905	GRLEWIFRRVLVYRPLQIFGQIPLDEIDBARNGSLHPLLEDSSASCPLVIANMLVILLL	964
QY	960	VTFLLVTVLMLNLLIAMFSYTFQVVOGNAITFMKFORNYLIVEHNEPALAPRILILSH	1015
Db	965	VTFLLVTVLMLNLLIAMFSYTFQVVOGNAIDFMKFORNYLIVEHNEPALAPRILILSH	1022
QY	1020	LSLTLRVYFKKAEKREHLEHDLDPDQKVVTVETVQKCNFLSKMEKRRRDSGEVYLR	1079
Db	1025	LSLTLRVYFKKAEKREHLEHDLDPDQKIIITWETVQKCNFLSTWEXRRRDSKEVYLR	1084
QY	1080	KTARHVDIATYKGLREOEKRIKCLBEOQINCSUVSVADVLAQGGPRSSQHCCEGS	1135
Db	1085	KTARHVDIATYKGLREOEKRIKCLBEOQANCMILSSMTDTLAPGGYSSSQHCGRSS	1144
QY	1140	QLVADHREGIDGWEQOPAGOPSPDT	1165
Db	1145	QPASARDR-----EYLEAGLPHSDT	1164

```

; FILE REFERENCE: A-71335-2/RFT/NBC
; CURRENT APPLICATION NUMBER: US/10/442,649
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/351,938
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1214
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-142-649--2

```

Query Match	39.9%	Score 2430.5	DB 12	Length 1214
Best Local Similarity	45.4%	Pred. No. 3.9e+216		
Matches 532	Conservative 177	Mismatches 352	Indels 111	Gap 26
Qy	26	GEVNFSGSGKKRGKRVAVPSGAVSVLPFDLLLAEMHLPAENLVVSLVGEEDPFAKMSWLR	85	
Dy	76	GEIDPFTAGRGKHSNPLRLSDRDTDAAYSLVTRTWGFRAPMLVVSVLGSGGAPVLTQWLDQ	135	
Qy	86	DVLRKGLVKAAOSNGAMITLSALVGLABHGAQVROHSLASTSTKRVAVVAGMASLGRV	145	
Dy	136	DLNRKGLVRAAQOSTGAWIVTGGLTGTGRHGVAVRDRHQMASTG-GRKVAVMGAPWGVV	194	
Qy	146	LHRRILIEAEDPFPVHY-PEDDSGSGQPLCSLSDNLSHFLIVBEGPAGKDGTEL	200	
Dy	195	RNRDTLINPKGSPFARYRMGDEPD--GVQPR--LDVNTSAFFLVDTGTHGCLGGENRF	249	
Qy	201	RLRLKXKISEORAGYGGTSGIETIVCLLVNGDPNTLTERISRAVEQAPMLVLVSGGTA	260	
Dy	250	RLRLIESYISQOKTGVGGTG-IDIVLLLLLDGDKMLTRLENATQAPLCLLVVSGGAA	308	
Qy	261	DVLAALVNOPHLVP-----KVAEKQFEKPSKHFMSWEDIVRWTLCLONITSHQHL	313	
Dy	309	DCLAETLED--TLAPSGGARGARORIRRFPK-----GDLEVLQOVERIMTRKLL	361	
Qy	314	TVYDFEEDGSEELDTVLKALKVAKCKSHSOEPODYDELKLVAMDRAVDIAKSEIFNGDV	373	
Dy	362	TVYSSE-DGSEEFETIYLVKALKVKAC--GSSEASAYLELRLAVAMNRVDIAQSELFRGDI	418	
Qy	374	EWKSCDLEEVWVDLVNKKPEFARLTFDNGADVADPLFTYGGLOGLYNSVSKULLFDLQ	433	
Dy	419	QMRSFHLASLMDLNDPREFVNLISHGISCHLFTPKMLADLYSAPNSLSLRLLD	478	
Qy	434	RKOEARLTLAGL--GTQOAREPPAGPAPSLHEVSVLVKDFLODACRPFYODGPRGDR	491	
Dy	479	QASHSACTKAPALKGAAELRPP-----DVGHVLRMLDKMCAPRRPSGGAMPH	528	
Qy	492	RAEKGPAKRTTGQKMYLIDLNOKS-----ENPRDPLFLMAYLVQNRHEATTFWAMGQ	542	
Dy	529	-----PQGFGESEWYLLSDKATPSLSLDAGLGQAPWBDLLMLALLNRQAQAMFWEMGS	583	
Qy	543	EGVAAALAAAKIKEMSHLLETEAARATREA--KYRLALDLDFSECSNSEAFAFALLV	600	
Dy	584	NAVSALGACULLLRVMARLEPDAEELARRKDLAKPFMGVCVDLGECCRSSEVAAARLL	643	
Qy	601	RNRKCSKTTCLHLATADAKAPPAHDGVQAFLTRITWGDMAAGTPILRLGAFVCFALV	660	
Dy	644	RRCPLMDATCLOLAMDARAFPAQOVOSLLPOKMMGDMASTPIWALVLAFFCPLI	703	
Qy	661	YTNLITE--SEEARPLRTGLEDLODLDLDTBKSPYLVLGQSRVEELVEAPRQSD-----	712	
Dy	704	YTRLITRKSEEBETREEL--EDMDSVINGEGFVGADPAEKTPFLGVPROSGAPGCCGG	761	
Qy	713	--RGPRAVFLITRWKRWGA.PVTVFLGNVVMYFAFLFTYVILLVDRPRPQSGSEVY	770	
Dy	762	RCGGRRC---LRWFHFMGAPVITFMGNVVSYLFLTLFSRVLLVDFOAP--FGSLELL	816	
Qy	771	LYFMVFLVLEELROGFTEDETF-----HLVKKFTLVYGDMMWNCMDVAIFLEI	819	
Dy	817	LYFMATFLCEELVQSGGGSGLASGGPGRGHASLSQRRLVLYADSNQCDVALTCFL	876	

QY 820 VGVTCRMLPSAEAGRTVLANDFMVFTLRLIHI PAIHKOLGPKIIVERMMKDVFFPLFF 879
 DB 877 LGVGRRLTFLGLYHIGRTYLCIDFMVFTYRLIHI FTVNQOLGPKIYIVSGMMKDVFFPLFF 936
 QY 880 LSVWLVAAGVTTQALLHPHDLGLEMIFRRVLYRPLYQIFGQIPDEIDEARV--NCSTH 936
 DB 937 LGVWLVAAGVATEGLLRPRDSDPFSILRRVFRPLYQIFGQIPQEDMDVALMEHNSCSSE 996
 QY 937 PULLEDSP-----SCPSLYANMLVLLVLTPLVJNNVLLMMLIMFSYTPQVGNATM 991
 DB 997 PGMFMAPGQAQAGTQVSOYANMLVLLVLTPLVJNNVLLMMLIMFSYTPQVGNATM 1056
 QY 992 FMKFORVNLIVYEHRRPALAPPFILLSLTLRRVFKK-----EAEHREHLEBD 1042
 DB 1057 YMKARVRLIRFHRPALAPPFIYISHRLRLRQICRRPRSPQSSPALHFRVYLSKE 1116
 QY 1043 LPDPLDQVVTWETVOKENFLSKMEKRRRDSGEVLRTKTAHVDPLAKYLSGLRQEKRI 1102
 DB 1117 ---AERKLLTWESYHKNFLLARADKRESDESERLKRTSQKVDLALKOLGHIREFEORL 1172
 QY 1103 KCLSEQINVCVSVSVADVLAQ-----GGR 1129
 DB 1173 KVLREVOQCSKVLGVMVAELSRALLPPGGR 1204

RESULT 7

US-09-789-481C-2
 ; Sequence 2, Application US/09789481C
 ; Patent No. US20020142377A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria Alexandra
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Lora, Jose M.
 ; TITLE OF INVENTION: 18607, A No. US20020142377A1el Human Calcium Channel
 ; FILE REFERENCE: MNI-097CP3
 ; CURRENT APPLICATION NUMBER: US/09/789,481C
 ; CURRENT FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 09/510,706
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 09/634,669
 ; PRIOR FILING DATE: 2000-08-08
 ; PRIOR APPLICATION NUMBER: 09/583,373
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1083
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-09-789-481C-2

Query Match 38.3%; Score 2335; DB 10; Length 1083;
 Best Local Similarity 45.7%; Pred. No. 2.5e-207;
 Matches 513; Conservative 165; Mismatches 338; Indels 106; Gaps 25;

QY 39 KTVRVSSGAPSVLPDLLAEMLPAPNIVSLVGEQPFAMKSWLRDVLKGLVYAAQS 98
 DB 4 QFLRLSDRDPDAVSLVTRTWGFRAPNIVSVLGGSGGVLTQWLDLRLKGLVYAAQS 63
 QY 99 TSMILTSALRVGLARHVGAVDHSLASTSTKRVVAVAGMASLGLVLRRIIEAODEP 158
 DB 64 TGMITVGLHIGLHGVAVADHOMASNG-CTKVAVAGVAVRWRRDITLANKGSF 122
 QY 159 PVHY-----PEDDGSQGLPCLSDLSLHFLIVEPGRPGKDGTLRLRLEKHISEORA 213
 DB 123 PARYWRGDPED--GVQFP---LDVYVSAFVLVDGTHGCLGSENFRLRLSEYISQOKT 177
 QY 214 GVGCTSSIRPVLCILVNDGPRNTERISAVEQAAWLLIVGSGGADVLAALVNGPHL 273
 DB 178 GVGCTG-IDIVLLLLIDGEEKLTRIENATQALPCLLVAGSGGADCAETLED--TL 234
 QY 274 VP-----KVAEKQPEKPPSKGFPMEDIVRWTKLLQNTTSQHLLTVVDFQESSEET 326

DB 225 AFGSGCAQGEABDRIRRFPPK-----GDLEVLQAOVERIMTRKELLTVYSSE-DGSEEF 288
 QY 327 DTVLKALVYKCKSHSQSPODYLDLKLAVAMDVRDIKSEIFPNQDVEKSCDLEBEVMD 386
 DB 289 ETIVKALVYKCK--GSSASAYLDELRLAVAMNRDILQSELFREDIDWRSHLEASLMD 346
 QY 387 ALVSNKPEFVRLFVNDGADVADFLTYGRLQELIYRSVSKSLFDLLQKQEBARLTLGL 446
 DB 347 ALLNDRPEFVRLLSHGSLGHFLTPMKRLAQYSAAPNSILRLNLLDQASHAGTAPAL 406
 QY 447 --GTQAAEPGAPPAFSLHEYSRLKDFLQDAGCGFTQDGRPGGRRAEKGPAPRPTQ 504
 DB 407 KGAAGELRPP-----DVGHVLRMLGKMCAPRPSGGAMPB-----PGGFGES 451
 QY 505 KMLDLNQS-----ENPMRDLFMAVLQNHENATYFAMAGQGEVAAALAAKIL 555
 DB 452 MYLLSDKATSPSLDAGLGQAPVMSLLMALLINRAQAMTFWENGSAVASALACILL 511
 QY 556 KEMSHLETEAEARATREA--KYERIALDLFSECYSNSBARAFALLVRRNCWSTTCLH 613
 DB 512 RVMARLEPDAEBAARXKOLAFKFEQGVLDLFCECYRSEVRARLLRRCPIMGDTCLQ 571
 QY 614 LATEADAAQFPAHGVQAFRLTRIMWGDMAAGTPIRLGALFCFALVYTNLITP--SEBA 671
 DB 572 LAMQADARAFPAQDQVOSLITQXWGDMASTPIWALVAFPCPLIYTRLITFRKSEEE 631
 QY 672 PLRTGLELDLQDLSLDTKSPLYGLQSRVEELVEAPRAQGD-----RGPRAVFLTR 723
 DB 632 PREELE--FMDDSYINGBPVGTADPAKPTPLGVPRQSGRGCCGCGGRRC--LRR 686
 QY 724 WRKFGAPVTVFGLGVNVMYFAFLFLTYVLLVDFPRPPGSGSPRETVLTFVFTVLBEI 783
 DB 687 WFFWGAQPTIFMGVNVSTLFLFLFSRLVLDVQPAR--PESLELLYFMAFTLLCEBL 744
 QY 784 ROGFTEDEPT-----HLVKKFTLYGDDNNKCDMAVIFLPIYGVTCRMLPSAE 832
 DB 745 RQGLSGGGGSLASGPGRGHSLSQRLRLYADSNMOCDLVALTFLGLVGGRLLPGLVH 804
 QY 833 AGRTVLANDFMVFTLRLIHI PAIHKOLGPKIIVERMMKDVFFPLFFLSVWLVAAGVTTQ 892
 DB 805 LGRVLCIDFMVFTYRLIHI FTVNQOLGPKIYIVSGMMKDVFFPLFFLGWLVAAGVATE 864
 QY 893 ALLHPHDLGLEWIFRRVLYRPLYQIFGQIPDEIDEARV--NCSTHPLLEDSP----- 944
 DB 865 GLLRPRDSDPFSILRRVFRPLYQIFGQIPQEDMDVALMEHNSCSSEPFMAHPQAQAG 924
 QY 945 SCPSLYANMLVLLVLTPLVJNNVLLMMLIMFSYTPQVGNATMFKFORVNLIVY 1004
 DB 925 TCVSQYANMLVLLVLTPLVJNNVLLMMLIMFSYTPQVGNATMFKFORVNLIVY 984
 QY 1005 HERPALAPPFILLSLTLRRVFKK-----EAEHREHLEBDLPDLDQKVWTE 1055
 DB 985 HSRPALAPPFIYISHRLRLRQICRRPRSPQSSPALHFRVYLSKE---AERKLLTWE 1040
 QY 1056 TVQKENFLSKMEKRRRDSGEVLRTKTAHVDPLAKYLSGLRQEKRI 1097
 DB 1041 SVHKNFLLARADKRESDESERLKRTSQKVDLALKOLGHIREFEORL 1082

RESULT 8

US-10-153-244-104
 ; Sequence 104, Application US/10153244
 ; Publication No. US20030144191A1.
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, TRP-2L
 ; TITLE OF INVENTION: SPLICE VARIANTS THEREOF
 ; FILE REFERENCE: D0144 NP
 ; CURRENT APPLICATION NUMBER: US/10/153,244
 ; CURRENT FILING DATE: 2002-05-22
 ; PRIOR APPLICATION NUMBER: US 60/292,599
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/362,944

PRIOR FILING DATE: 2002-03-08
 NUMBER OF SEQ ID NOS: 335
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 104
 LENGTH: 1503
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-153-244-104

Query Match 33.5%; Score 2041; DB 12; Length 1503;
 Best Local Similarity 38.8%; Pred. No. 9,66-180;
 Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

26 GEVNFSGGKRGKGFVAVPSVLPDLLEAEMLPAPLVSLVGEOPFAMKSWLR 85
 128 GDIVFTGLSQKVKYVVSQDTPSSVITYHMTQHMGLDVPNLLISVTGAKFNFKPRLK 187
 86 DVLKRGVKAASOTAMITLSARVGLARHVGQARHDSLASTSTKRVAVAGMASLGRV 145
 188 SIFRRGLVKAQTTGAMITIGSGHTGVKMGVEAVRDPSSSYKEGELITIGAVTWTQV 247
 146 LHRRILEAEQEDFVPHYEPEDDGSQGPLCSLDNSHFIIVBPGPKGDDLTLELRLE 205
 248 HRREGLIHPTGSPFAEYILDEBG--QGNLTCLDSNHSFIIVDGTGQYGEIPLRTLE 306
 206 KHISQRAQYGGTSGIEIPVLCCLVNGDPNTLERISRAVEQAPWLLVSGSGIADVLAA 265
 307 KFISQTERKGGV-AIKIPIVCVLEGGGTLHTIDNATTTNGTPCVAVGSGRADVIAQ 365
 266 LVNQP--HLVPKVAEKQ---FKKFPKSHFMSWDIYRWKTLQNTSHQHLITVYDEQ 320
 366 VANLPVSDITISLQOKLSVFPQEMFET--FTESRIYEWTKKIDIVRRQLLTVPREGK 423
 321 EGSEELDTVILKALVKACKSHSQEPODYLD--ELKLAVAMRDVIAKSEIFNGDVEMKSCD 379
 424 DGQODVVAILOALLKASRSQDHFGHEMNDHOLKLAANMRVDIARSEIFNDEMOMKPSD 483
 380 LEEVNVDAIVSNKPEFVRLFVNDGADVADFLTYGRLQELYSVSRKSLFDLLQKQKEA 439
 484 LHPMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLENLDPSCLFHSKLQK----- 538
 440 RLTLAAGLTQQAAREPAGP--PARSLHVSRYLKQFLDQACRGFYQDGRPGDRRR----- 492
 539 -----LVDEPERACAPAAIRLOMHNVAQVLRBELDQFQPLRPRRHNDRLLLPV 592
 493 -----AEKGAKRPTGOKWLLDNOKSENPMRDLFMAVLONHEMATTYWMAGQ 542
 593 PAVKLVNCGVSLRSGLYKSSGSHVT-----TMDPIRDLILWAIYONRRELGLIIMASQ 646
 543 EGVAAALAAKILKEMSHLETEAAR--ATREAKYERLALDLFSECYNSSEARAFALL 599
 647 DCIAAALLCKSLIKELSEBEDTDSSEMLALAE-EYENRAIGVTECYRDEBAQKLL 705
 600 VRRNRCKSTCTCLHATEADAKAFADHGVQAFLTRIWMGMAACTPILRLIGAFLCAL 659
 706 TRVSAMWKTCTCLALAEAKMKFVSHGIIQAFILTKVMGQSLVNGIMRVTLLCMLAPL 765
 660 VYTNLITSEEARLRTGLEDLODDSLDTEKSPILGLOSVEBELVEARAGDRPRAVF 719
 766 LITGLISREK-----LQD-----VGTAA----- 786
 720 LLTRKRFMGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPGSGSEVTLFYVFTLV 779
 787 ---RARAFAPVAVVFNHILISYFAFLCPAVLVMDQPV---PSWECALYIMLFSLV 840
 780 LEEIRQGFTEBDTHLVKFTLVYGDNNKCDMAVILFPIVGTGRMLPSAEAGRTVLA 839
 841 CEEMKQFLYDDECEIMKKAALYFSDFMNKLDVGAILLFFVAGLTCRLIPATLYPERVILS 900
 840 MDPMVFTRLIIFAIHKOLGPKIIVERRMKDVEFEFLFSVMTVAAGVTTOALLHHD 899
 901 LDFILFCRLMHIIFITISKTLGPKIIVRRMKDVEFEFLFLAVVWVSFGVAKOALLHNE 960

900 GRLEWIFRRVLYRPLQIFQIP--LDEIDEARVNC--THPLLEDSPSCPS----- 948
 961 RRVDMLFRGAVYHSYLTIFQIDGVNFPNPSCHNGTDPY---KPKCSBDATQ 1016
 949 --LYANNVILLITVLTNVLNMLLIAMFSTTFQVQGNAMTFKFGYRNLIVEYHE 1006
 1017 RPAPPEWLTVLLLTCLYLLFTVILLNLIAMFNFTFOVDEHTDOIMFQSHDLIEEYHG 1076
 1007 RPALAPPEILSHSLTLRVRVFKKEAEKREHLEERDLPDLQKVTWETVOKENFISKM 1066
 1077 RPAPPEILSHSLQFLTKRVVLTAKRKHQKKEKEEADLSMEIYLVKENYLONR 1136
 1067 EKRRRDSEGLVARTAHRVDFIAYL-----GGLREDEKRIKLESQINYSVLVS 1118
 1137 QFOQKQREKQKIEDISNKVDAMVLDLDPKRSQSM---EQRLASLEQVAAQARALHM 1193
 1119 VADVLAQCGPRSSQHCQESQVLAAD---HRGIDGHEQPG 1157
 1194 IVRTLRAQSGFSSSEADVPPLASQKAAEBDAPRGKRTKEBPG 1235

RESULT 9

US-10-210-152-21
 ; Sequence 21, Application US/10210152
 ; Publication No. US20030162189A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, LTRPC3
 ; FILE REFERENCE: D0171 NP
 ; CURRENT APPLICATION NUMBER: US/10/210,152
 ; PRIOR FILING DATE: 2002-08-01
 ; PRIOR APPLICATION NUMBER: US 60/309,544
 ; NUMBER OF SEQ ID NOS: 320
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 21
 ; LENGTH: 1503
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-210-152-21

Query Match 33.5%; Score 2041; DB 12; Length 1503;
 Best Local Similarity 38.8%; Pred. No. 9,66-180;
 Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

26 GEVNFSGGKRGKGFVAVPSVLPDLLEAEMLPAPLVSLVGEOPFAMKSWLR 85
 128 GDIVFTGLSQKVKYVVSQDTPSSVITYHMTQHMGLDVPNLLISVTGAKFNFKPRLK 187
 86 DVLKRGVKAASOTAMITLSARVGLARHVGQARHDSLASTSTKRVAVAGMASLGRV 145
 188 SIFRRGLVKAQTTGAMITIGSGHTGVKMGVEAVRDPSSSYKEGELITIGAVTWTQV 247
 146 LHRRILEAEQEDFVPHYEPEDDGSQGPLCSLDNSHFIIVBPGPKGDDLTLELRLE 205
 248 HRREGLIHPTGSPFAEYILDEBG--QGNLTCLDSNHSFIIVDGTGQYGEIPLRTLE 306
 206 KHISQRAQYGGTSGIEIPVLCCLVNGDPNTLERISRAVEQAPWLLVSGSGIADVLAA 265
 307 KFISQTERKGGV-AIKIPIVCVLEGGGTLHTIDNATTTNGTPCVAVGSGRADVIAQ 365
 266 LVNQP--HLVPKVAEKQ---FKKFPKSHFMSWDIYRWKTLQNTSHQHLITVYDEQ 320
 366 VANLPVSDITISLQOKLSVFPQEMFET--FTESRIYEWTKKIDIVRRQLLTVPREGK 423
 321 EGSEELDTVILKALVKACKSHSQEPODYLD--ELKLAVAMRDVIAKSEIFNGDVEMKSCD 379
 424 DGQODVVAILOALLKASRSQDHFGHEMNDHOLKLAANMRVDIARSEIFNDEMOMKPSD 483
 380 LEEVNVDAIVSNKPEFVRLFVNDGADVADFLTYGRLQELYSVSRKSLFDLLQKQKEA 439
 484 LHPMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLENLDPSCLFHSKLQK----- 538

```

QY 440 RLTLAGTGOAREBPAG--PASFHEVSRYLKDPLDADACGFGYODGPGRRR----- 492
Db 539 -----VLVEDEBERACAPARBLDMHVAQVRLRELDFTQPLYPRRHRDLRLLPV 592
QY 493 -----AEKGAKEPTGOKMLLDNOKSENPMRDLFLMAVLONRHEMATYWMAGQ 542
Db 593 PHVKLVNOGVSRLSYKRSSSHVT-----TMDPIRDLRLMAIQNRRELGLIWAOSQ 646
QY 543 BGVAAALAACTIKKMSHLETAEAR--ATREAKYERLALDLFSECSNSAQAFAILL 599
Db 647 DCIAAALACSKILKEISEEDTDSSEMLALAE-EYEHRAIGVFTECRKDEBAOKXL 705
QY 600 VRNRNCSWKTCLHATEADAKAFPAHDGVOAFLTRIMGDMAGTPILRLGAFELCFAL 659
Db 706 TRVSAMGKTTCLOLALBAKMKFVSHGIGQAFUTKVMWGQSLVNDGLMRVTLCLAPFL 765
QY 660 VYTNLITSEEARPLRTGLELDLQDLSLDTESPLYGLOSVELEVEAPRAODGRPAVF 719
Db 766 LITGLISFEKRA-----LQD-----VGTAA----- 786
QY 720 LITRRKFMGAQVUTYFLGNVVMYFAFLFTYVLLVDRPPRPGSGPEVTLYFWVFTLY 779
Db 787 ---RARAFPTAVVVFHNLISYFAFLCLFAYLVWDFQPV---PSWCECATYMLFSLV 840
QY 780 LEEIRGFEPTDETHLVKKFTLYVGDNNMKCDMAVIFLIVGTCRMLPSAEAGRTVLA 839
Db 841 CEEMQOLFYPDECGIMKKALYFSDFMKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
QY 840 MDMVFTLRLIHIFAIHQOLGPKIIVBERMKDVFFFFLFSVWLVAAGVTTOALLHPD 899
Db 901 LDFILFCLRLMHIFTISKLGPKIIVKRMKDVFFFFLAVVWSFGVAQAILIHNE 960
QY 900 GLEWIFRRVLYRPLQIFGOIP--LDEIDEARVNS---THPLLEDSPPSPS----- 948
Db 961 RRVDWLFPGAVHSHLTITFGQIPGYIDGVNFBHSPNGTDPY---KPKCPESDAAQO 1016
QY 949 --LVANMVLVILLVFLVTVNLVNLMLIAMFSYTFQVVOGNATMFWKFORNLYVEYHE 1006
Db 1017 RPAPEWLVLLVLCYLLTNTLNLMLIAMFNNTYFOOVBEHTDOIWKFORIDLIEYHG 1076
QY 1007 RPAAPRPFILSHLSLTLLRVRVEKKEAENKREHLERDLPDLQKVVTWETVOKENFLSKM 1066
Db 1077 RPAAPRPFILSHLDLFIKRVVLTKPRAKNHQLKNLEKNEBALSWETIYUKENYLOVR 1136
QY 1067 EKRRDSEGEVUKTAHRYDFTAKYL-----GGLREOEKIKLESQIYCSVLVSS 1118
Db 1137 QFOOKORPEOKIEDISNKVADAVDLDLDPKRSQSM---EORLASLEBOVAQOTARALHM 1193
QY 1119 VADVLAOGGPRSSOHCSEGSQLVAD---HRGGIDGWEOPG 1157
Db 1194 IYRTLRASGFSSEADVPTLASOKAAEERPAEFGGRKTEEPG 1235

RESULT 10
US-10-007-706-1
; Sequence 1, Application US/10007706
; Publication No. US20020182635A1
; GENERAL INFORMATION:
; APPLICANT: Penner, Reinhold
; APPLICANT: Fleisig, Andrea
; TITLE OF INVENTION: METHODS OF SCREENING FOR LTRPC2 MODULATORS
; FILE REFERENCE: A-70040-1/RTF/NBC
; CURRENT APPLICATION NUMBER: US/10/007,706
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,442
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/254,528
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1503

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-706-1
Query Match      33.5%; Score 2041; DB 14; Length 1503;
Best Local Similarity 38.8%; Pred. No. 9,66-180;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGSKKRGKRVVRPSGAPVAPFLDLLAEWHLPAPNLVVLVEGEOPFAKSMWR 85
Db 128 GDVFTGSLQYKXIVRVSQDTPSSVYTHMTQHGKGLVPMNLISVTGAKAFNKKPRLK 187
QY 86 DVLRKGLVKAAGSTGAMITLSALRVGLARHVGQAVRDSHLASTSTKRVAVAGMASLGRV 145
Db 188 SIFRGLVKAQVOTTGAWIITGSHTGVMKQGEAVRDSLSSTSSYKEGLITITGATWGTV 247
QY 146 LHRRLIEAQEDFPNHYPEDDGSGPCLSDNSINSHILVEPFGPGDGLTELRLE 205
Db 248 HRREGLIHPTGSFPFEXYLLDBDG--QGNLTCLDSNHSFILVDDGTHGGVGEIPLRTLE 306
QY 206 KHISQORAGYGGTGSEIPVLCCLVNGDPNTLERISRAVEQAAPMLLVGSGGIADVLAA 265
Db 307 KFISEQTERGAV-AIKIPIVCVLEGGPGILHTIDNATTTGCTPCVVEGSGRVADVIAQ 365
QY 266 LVNQP--HLVPKVAEKQ---FKKFKPSKHSWEDIVETKLLQNTSHQHLITVYDFEQ 320
Db 366 VANLPVSDITISLIQKLSVFQEMFET--FTESRIVEWTKKIDIVARRQLLTIVFRBGK 423
QY 321 EGSEELDVILKALVYKAKSHSOEPDYLD--ELKLAVAMDRVDIAXSEIFNGDVWKKSCD 379
Db 424 DGQODVVAIIQALIKASRSODHFGHEWMDQLKLAVAMNRVDIARSEIFNDEMOMKPSD 483
QY 360 LEEVWVDALVNNKPEFVLFVONGADVADPLTYGSLQELYSVSRSKSLFLDLOKOEBA 439
Db 484 LHPITTAALISVKEPEVLFLENGVQLKEFTWDTLLTYENLUDSCIFSHSLQK----- 538
QY 440 RLTLAGTGOAREBPAG--PASFHEVSRYLKDPLDADACGFGYODGPGRRR----- 492
Db 539 -----VLVEDEBERACAPARBLDMHVAQVRLRELDFTQPLYPRRHRDLRLLPV 592
QY 493 -----AEKGAKEPTGOKMLLDNOKSENPMRDLFLMAVLONRHEMATYWMAGQ 542
Db 593 PHVKLVNOGVSRLSYKRSSSHVT-----TMDPIRDLRLMAIQNRRELGLIWAOSQ 646
QY 543 BGVAAALAACTIKKMSHLETAEAR--ATREAKYERLALDLFSECSNSAQAFAILL 599
Db 647 DCIAAALACSKILKEISEEDTDSSEMLALAE-EYEHRAIGVFTECRKDEBAOKXL 705
QY 600 VRNRNCSWKTCLHATEADAKAFPAHDGVOAFLTRIMGDMAGTPILRLGAFELCFAL 659
Db 706 TRVSAMGKTTCLOLALBAKMKFVSHGIGQAFUTKVMWGQSLVNDGLMRVTLCLAPFL 765
QY 660 VYTNLITSEEARPLRTGLELDLQDLSLDTESPLYGLOSVELEVEAPRAODGRPAVF 719
Db 766 LITGLISFEKRA-----LQD-----VGTAA----- 786
QY 720 LITRRKFMGAQVUTYFLGNVVMYFAFLFTYVLLVDRPPRPGSGPEVTLYFWVFTLY 779
Db 787 ---RARAFPTAVVVFHNLISYFAFLCLFAYLVWDFQPV---PSWCECATYMLFSLV 840
QY 780 LEEIRGFEPTDETHLVKKFTLYVGDNNMKCDMAVIFLIVGTCRMLPSAEAGRTVLA 839
Db 841 CEEMQOLFYPDECGIMKKALYFSDFMKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
QY 840 MDMVFTLRLIHIFAIHQOLGPKIIVBERMKDVFFFFLFSVWLVAAGVTTOALLHPD 899
Db 901 LDFILFCLRLMHIFTISKLGPKIIVKRMKDVFFFFLAVVWSFGVAQAILIHNE 960
QY 900 GLEWIFRRVLYRPLQIFGOIP--LDEIDEARVNS---THPLLEDSPPSPS----- 948
Db 961 RRVDWLFPGAVHSHLTITFGQIPGYIDGVNFBHSPNGTDPY---KPKCPESDAAQO 1016
QY 949 --LVANMVLVILLVFLVTVNLVNLMLIAMFSYTFQVVOGNATMFWKFORNLYVEYHE 1006

```


Db 1017 RPAPEWMTLVLLCLYLLFTNLLNLINLIFAMFNNTFOQOEFTDOIWKFORDLLEHYG 1076
Qy 1007 RPAALPELILSHLSLTLRVFEKEAENKREHLERDLDPDLQKVWETVOKENFLSGM 1066
Db 1077 RPAAPPELILSHLDLFTIKRVVLKTPAKRHOKKLEKNEAALLSMETIYKENYLONR 1136
Qy 1067 EKRRDSEGEVLRTKAHRVDFTAKYL-----GGLREQEKRIKLESQIYCSVLVS 1118
Db 1137 OFOQOEKREKIEDISNKVDAMVDLLDPLKRSISM---EQLASLEQVAVQTRALHW 1193
Qy 1119 VADVLAAOGGRRSSQHCESQLVAD--HKGIDGMEQPG 1157
Db 1194 IVTRLASGFSSEADVPTLASQAAEPDAEPGRKKEEPG 1235

RESULT 11
US-10-171-319-8
Sequence 8, Application US/10171319
Publication No. US20030157633A1
GENERAL INFORMATION:
APPLICANT: Ardem Patapoutian
APPLICANT: Andrea Peier
APPLICANT: Peter McIntyre
APPLICANT: Stuart Bevan
APPLICANT: Chuanzheng Song
APPLICANT: Pamosh Ganju
TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: AND POLYPEPTIDES
FILE REFERENCE: 4-32048A
CURRENT APPLICATION NUMBER: US/10/171,319
PRIORITY FILING DATE: 2002-10-24
PRIORITY APPLICATION NUMBER: 60/297,835
PRIORITY FILING DATE: 2001-06-13
PRIORITY APPLICATION NUMBER: 60/351,238
PRIORITY FILING DATE: 2002-01-22
PRIORITY APPLICATION NUMBER: 60/352,914
PRIORITY FILING DATE: 2002-01-29
PRIORITY APPLICATION NUMBER: 60/357,161
PRIORITY FILING DATE: 2002-02-12
PRIORITY APPLICATION NUMBER: 60/381,086
PRIORITY FILING DATE: 2002-05-15
PRIORITY APPLICATION NUMBER: 60/381,739
PRIORITY FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1104
TYPE: PRT
ORGANISM: Mus musculus
US-10-171-319-8

Query Match 25.9%; Score 1578; DB 12; Length 1104;
Best Local Similarity 33.4%; Pred. No. 6,5e-137;
Matches 374; Conservative 207; Mismatches 392; Indels 148; Gaps 24;

Qy 26 GENVNGSGKKRGKRVVPSGVAAPSVLFDLLAEWHLPAPNVYVLSVEEDQEFAMKSLR 85
Db 104 GDIOPEITLGGK-GKTLRLSCDTSETLYELLTQHWHLTPNLVLSVGTAKNFAKPRMR 162
Qy 86 DVLRKGLVKAQSTGAWILTSALRVGLARHVGQAVRSHSLASTSTKRVVAVGMASLGRV 145
Db 163 KIFSR-LIYIQAQSKAWILTGTHGLMKYIGEVVNDMTI-SRNEENIIVAGIAMGV 220
Qy 146 LHRRLIEAQRD--FPHYEPEDDGGSGPLCSLDSNLSHTLVEGPGKDGTLERL 202
Db 221 SNRPTLRSQDEGFAQYIMDD-FTRDPLYILDNNHTHLVYDNGCHGHPVEAKLRN 279
Qy 203 RLEKHSIE--ORAGYGTGSIETIPVLCILVNGDPNTERISRAVEQAAPWLLVSGSGI 259
Db 280 QLEKISRTSDSNVYG---KPIVFPAGGGGHEITKAIINTSVKSIPICVVVGSGOI 335
Qy 260 ADVLAALVNPPLLVPKVAEKQFKEKFP--KHFSWEDIIVWTKLQNTISHOHLTVYD 317

Db 336 ADVIASIVEVDVLTSSWKEKLVRFLEPRTVSRLPEEIEBSWIKWLESSHLLTYIK 395
Qy 318 FEOGSEEDLVYILKALVACKASHQOEQDYLDELKLVANDRVDAIASEIFNGEVKMS 377
Db 396 MEAGDEIVSAISYALYKASTNEQDKONNGQKLLLENNQDLDADEFTNDRWES 455
Qy 378 CDLEEVVDALVSNKPEFVRLFVNGADVADPFLTYGRLOEYRSVRSKSLFDLLQ---R 434
Db 456 ADLQVMTALIKORPKRVRLFLENGNLQKFTLNEVTELF-SHFSTLYRNQIAKN 514
Qy 435 KOBEARLTLAGLGTQOAREPAPGAPFSLHEVSRVLPLODACGFYQDGRPGDRRAE 494
Db 515 SYNALLTF-----VMKLVANFR-----RSFWKEDR----- 540
Qy 495 KGPARKPTGQKMLDLNOKSENPWRDLFLMAVLONRHEMATYFPMAGOEQVAAALAAKI 554
Db 541---SSREDLVDELHDASTTRHPLOALEFVALILONKKELSVYIWEQTGCTLLAAGASKL 597
Qy 555 LKEMSHLETEAARATREA--KYERLADLFSECCYSSEBARAFALVRRNRCSKTCL 612
Db 598 LKTLAKVNDINNAQSESELANBYETRAVELFTECYSNDEDLAQLLVYSCBAGNSCL 657
Qy 613 HLATEADAKAFPAHDGVAFLTRIMGDMAGTPIRLLLGAPLCPALVYTNLITFSEAP 672
Db 658 ELAVEATDQHFIAQPGVQNFSLKOWYGBISRDYKWKILCLFLIPIVCGGLVSPKK-- 715
Qy 673 LRTGLDEDLQDLSIDTESPIYGLOSRYEELVEAPRAGDGRPAVFLITMKRWGAPV 732
Db 716-----PIDKHK-----LLWYVAFETSPF 735
Qy 733 TVPLGNVVPAPFLFTYVLLVDFRPPQSGPSEVTLFVWFTLVYEEIRQGFTEDE 792
Db 736 VFGSNVVFYIAFLILPARYVLLIMPHSVPH--TPELLVAVFLPCDEVRQMYMGVN 792
Qy 793 THLVKFFLVYGDWNNKDMVAIFLFTVGTCRM---LPSAFBAGRTVLANDFVFTLR 849
Db 793-----YETDLMNVMDTLGLFYIAGIYVRLHSSKSLSGRVIFCDYIIFTRL 843
Qy 850 IHIFAIKQOPKIIYVERMKVDYFFFLFSLVLYAVGVTQALLHHDGLKLEIFRRV 909
Db 844 IHIFVSRNLGPKIMQRMIDVFFFLPAAVNVVAFGARQGLRNEQRMWRIFRSV 903
Qy 910 LYRPLAIFGOIPDEIDEARVNS-----THPLLLE-DSPSCPSLVANMLITLLV 960
Db 904 IYEPYLMFGVPSD-VDSTTYDSHCTFSGNESEKPLCEVLEDEHNLPR-FPEWITIPVLC 961
Qy 961 TFLVTVLNLNLINLIFAMFSTFOVVGATFMFKFORNYNLIVEYHERPALAPPLILSHL 1020
Db 962 IYMLSTNILLVNLVAMFGYVGVIGENNDQVWKFQRYFLVQVQCNRLNIFFPFAVFAFV 1021
Qy 1021 SLTTRVYFKKAENKREHLERDLDPDLQKVWETVOKENFLSKMEXRRDSEGEVLK 1080
Db 1022 YMVVWKFCKCKCKKNESNACCFRNEBNETLAMEGWKENYLVKINTKANDNS----- 1075
Qy 1081 TAHRVDFTAKLGLRQEKRIKLESQIYCSVLVSVD 1121
Db 1076-----EEMRRHFRQDLSKLDLKSLEKIAN 1101

RESULT 12
US-09-759-143-778
Sequence 778, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.


```

; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepier, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-143-778

Query Match      25.7%; Score 1562.5; DB 9; Length 1095;
Best Local Similarity 34.2%; Pred. No. 1.8e-135;
Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

QY 26 GEVNGSGKRRGKRVVPSVLAFLPDLAELHMLPAPNLVSLVGEOPFPAKSMWR 85
DB 95 GDIOFTYLGK-GKYIRLSCDPAELVYLLTOHMLKPLNVLISVGAQKFAKPRMR 153
QY 86 DVLRLGLVKAQSTGAMITLALRVGLARHVGQAVHDHSLASTSTFKRVVAVGMAISLGRV 145
DB 154 KIFSR-LIYIAOSKAMITLGTHTGLTYIGEVARDNT-SRSEENVALGIANAMGV 211
QY 146 LARRILE--EAQEDFPVHYRPPDDGSGGCLSDNSLHFLVBERPPKGDGLTELR 202
DB 212 SNRDILIRNCDAEGYLAQYLMDD-FTRDPLYLIDNNHLLHLLVNDGCHGPTVEAKLKN 270
QY 203 RLEKHTISE--ORAGYGTGSIPIPLCLLVNDPRTLEIRISRAVGOAPMLIVGSGGI 259
DB 271 QLEKHSITTDSDNG--KIPVCPAOGGKETTIAINTSINKLPCVVBSGSKI 326
QY 260 ADVLAALVNQPHLVKVAEKFKEKFP--KHFSMEDIVRWTKLONITSHOHLITVVD 317
DB 327 ADVIATSLVEDEAPRTSSAVKEKLVRLPTVSRSLSEETESHIKMLKEITLCSHLITVAK 386
QY 318 FEQESSELDITVILKALVAKCSHSGEPDYLDELKLAVAMBRVDIAKSEIFNGDWMKS 377
DB 387 MEAGDEIVSNALISVALYKAFSTSEQDKUNMGQLKLLLEMQDLDEIFTNDRWES 446
QY 378 CLEEVMDVALVSNKEPFRLVNDGADVADFLTYRLOELYSVRKSLDLDLO--R 434
DB 447 ADLOEVMFALIKDRKFRVLENGLNLRKFLTHVLELF-SNHFSTLVRLNLIQIAN 505
QY 435 KOEBAKRLTAGLGTQOARPPAPRPAFSLSHEVSRVLDPLODACRFYDGGPRG-DRRA 493
DB 506 SYNDALITL-----VKLVANR-----KGRKEDRGRDBEMT 539
QY 494 EKGPARRPTGOKWLLDLNOKSEPMWDLFLMAVLONRHMAFYFWAMGEGVAAALAAK 553
DB 540 E-----LHDVSPITRHPLOALFIMAILQKKELSKYIMBOTRGCTLAALGASK 587
QY 554 ILKEMSHLETEAARATREA--KYERLLDLFSECTYNSSEARAFLLVRRKCMKTKC 611
DB 588 LKLTAKVNDINNAAGESEELANEYETRAVELFTECVSSDEDLAEBLLVYSCAEMGSGNC 647
QY 612 LHLATEADAKAFADGVQAFILRIWMGMAAGTPIRLIGAFLCFALVYVNLITSEBA 671
DB 648 LBLAVATQHTAQTGQVONFLSKQWYGEISRDTKMKIKIILFIPLVCGGCVSRKK- 706
QY 672 PLRTGLELDQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRPAVFLITRMRKFWGAP 731
DB 707 -----PVDKHKK-----LLWYVVAFTSP 725

```

```

QY 732 VTVFLGNVWYFAFLFTYVLVDFRPPPOGSGSEVTLFWFTVLEIRQGFIDE 791
DB 726 FVFSMNWVFYIARLFLRAYVLLNDHSHVPH---PPELVISLVFLVCFDEQRQYVNGV 782
QY 792 DTHLVKKEFLVGDNMNKCDAVAFLEIVGVTCRN--LPSAFAEGRTVLANDENVFTLR 848
DB 793 N+-----YFTDLMNWDTGLFEPFAGIVFRLHSSNKSLSYSGRAVIFCLDYIIFTLR 833
QY 849 LIHIFAIHKOQPKTIIVERMKOVFFELFSLVSLVAVGYTQALLPHORLEMRIR 908
DB 834 LIHIFTVRNIGPKTIMQRMIDVFFLPFAVMMVAFGARQILKONEQRMRWERS 893
QY 909 VLYRPLYOIFGOIPLDEIDEAR--VNCS-----THPLLE-DSBSCSLYANMLVILL 959
DB 894 VLYRPLYAMFGQVSD-VDGTTYDPAHCTFPGNESKPLCEVLEIDENLDR-FREWITIPLV 951
QY 960 VTFLVTVLNNLMLIANFSTYFOVVGNAITFMKFORNYLIVEYHERPALAPPTILSH 1019
DB 952 CIYMLSTWILLVNLVAMEGTVGVQENNDQVMKFORVFLVQESYSLNIPPEVIFAY 1011
QY 1020 LSLTRRVFKAEKREHLERDLPDLDOKVYTMETVOKENFSLKMKRRRDSGEVLR 1079
DB 1012 FYMVVKKGFCCKCKEKNNESSVCCFNEDNETLAWEGVMEKENVLVKINTKADT-SEEMR 1070
QY 1080 KTAHRVDFLAKYLG-LRQOEKRIK 1103
DB 1071 HRFRODTRKNDLKLKEINANKIR 1095

RESULT 13
US-09-780-669-778
; Sequence 778, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepier, William
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-780-669-778

Query Match      25.7%; Score 1562.5; DB 9; Length 1095;
Best Local Similarity 34.2%; Pred. No. 1.8e-135;
Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

QY 26 GEVNGSGKRRGKRVVPSVLAFLPDLAELHMLPAPNLVSLVGEOPFPAKSMWR 85

```

```

Db      95 GDIQFETLGGK-GKTYIRLSCDTDAEILYELLTOHMLKTPNLVISTVGAKNFALKPRMR 153
Qy      86 DVLRKGLVKAAGSTGAMILTSALRVGLARHVGQAVRDSLASTSTKRVVAVGMAISGRV 145
Db      154 KIFSR-LIYIAQSGAMILTGTHGLTKYIGEVVRNTI--SRSEENIYVAIGIAMGMV 211
Qy      146 LHRRL--EAQDFPVNHPEDDGGSGQLCSIDNSHFLVEPFGPKGDLTELRL 202
Db      212 SNRDTLLRNCAEGEFLAQYIMDD--FTRDPLVILDNHNTHLILDVNGCHGHPTEAKLRN 270
Qy      203 RLEKHISE--ORAGYGTGSIETPVLCVLVNGDNTLERISRAVEQAAPMLILVSGGI 259
Db      271 QLEKHISERTTODSNYGG---KIPVCPAOGGKETLKAINTSIKKIPCVVVEGSGRI 326
Qy      260 ADVLAALVNQPHLLVPKVAEKQFKEKPPS--KHFSMEDIVRWTKLQNTSHOHLITYYD 317
Db      327 ADVIASLVEEDAPTSSAVKEKLVRLPRVTSRLESEETESWIKMLKEILCSHLITVYIK 386
Qy      318 FEQSGSELDVTIILKALVKACKSHSQEPQDYLDLKLAVANDRVIAKSEIFNGDVEWKS 377
Db      387 MEEAGDEIVSNAISYALYKAFSTSEQDKNNNGQLKLLBNQDLANDEIFTNDRWES 446
Qy      378 CDLEEVWDAVLSNKEPFRVLPVNDGADVADPLTYGLOELVRSKSLFDLQ--R 434
Db      447 ADLQEVMTALIKRPFVRLFLENGLNRKFLTHDVLTELF--SNHSTVLVRYMLQIAKN 505
Qy      435 KOEBAFLTLAGTQOAREPPAPRPAFSLHEVSRLKDFLODACGFQDGRPG--DRRA 493
Db      506 SYNDALLTF-----VKLVANFR---RGRKEDRNGRDEMID 539
Qy      494 EKGPAKPTGQKWLIDLNQKSENPWRDLFLMAVLONRHENATYFWAMQOEGVAAALACK 553
Db      540 E-----LHDVSPITRHPLOALFIWAILONKKELSKVIMEQTRGCTLAALGASK 587
Qy      554 ILKEMSHLETAEAARATREA--KYERLADLFSCYCSNSBARFALLVRRNRCKSTTC 611
Db      588 LKTLKAVKNDINAAGESEELANEYETRAVELFTECYSDEDLAEQLLVYSCAMGSGNC 647
Qy      612 LHLATEADAKAFPAHDVQAFLTRIMGDMAGPILRLGALCFALVYTNLTFSSEA 671
Db      648 LELAVEATDQHTAQOPGVQNLFSKOMYGEISRTQKMKIILCFIPLVGGFVSFRKK- 706
Qy      672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRPAVFLTLTRMKFWGAP 731
Db      707 -----PVDKHKK-----LMWYVVAFTTSP 725
Qy      732 VTVEFLGNVWYFAELFLFTYVLLVDPRPPQSGSGREVTLVFWFTLVLEIRQGFETDE 791
Db      726 FVPSWNVVFIATFLFAYVLLMDFHSVPH---PPELVLVSLVFLFCDEVRQMYVNGV 782
Qy      792 DTHLVKKFTLVVGNMNCMDVVAIFLFIYVTCRM---LPSAFEGGRVVLAMDENVFTLR 848
Db      783 N-----FTDLMNVMDTLGLFYTAGIVFRLHSSNKSLSYSGRIYFLCLDIIFLRL 833
Qy      849 LIIHFAIHKQKPIIIVERMMKDVFFFLFSLVWLVAVYVTOALLPHDGRLEWIFRR 908
Db      834 LIHIFTYSRNLGPKIIMQRLIDVFFFLFLPAVMMVAFGVARGCILRQNGRMRMIFRS 893
Qy      909 VLYRPYQIFQOILDEIDEAR---VNCS-----THPILLE--DSPSCSLVAMNLVITLL 959
Db      894 VIYERPYLAMPQOVPSD--VDGTTYDFAHCTFNGNESKPLCEVLDEHNLPR--PREWITPLV 951
Qy      960 VTEFLVNVNLLMNLIMFSYTPQVONATMFWKFORVNLIVYHERPALAPFILLSH 1019
Db      952 CIYMLSTNILLNLVAMFGITVGTVDENNDQVMKFORFYLVQECSSNLPPFPIYFAY 1011
Qy      1020 LSLTLRAVFKKEAKHEHLERDLPDLQKVVTWETVQENFLSKMEKRRRDSGEVLR 1079
Db      1012 FYWVVKACFCCKCKEKNNESSVCCFKMEDNETTLAMEGVMKENYLVKINTKANDI--SEMR 1070
Qy      1080 KTAHRVDFIAKYLG--LREQEKRIK 1103

```

```

Db      1071 HRFQDLTKMLDKLLEKIANKIK 1095

RESULT 14
US-09-822-827-778
; Sequence 778, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-822-827-778

Query Match      25.7%; Score 1562.5; DB 9; Length 1095;
Best Local Similarity 34.2%; Pred. No. 1.8e-135;
Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

Qy      26 GEVNFSGGKRGKGFVBPSPVARSVLPFDLLAEMLPAPVLYSLVGEQEPFAMKSLR 85
Db      95 GDIQFETLGGK-GKTYIRLSCDTDAEILYELLTOHMLKTPNLVISTVGAKNFALKPRMR 153
Qy      86 DVLRKGLVKAAGSTGAMILTSALRVGLARHVGQAVRDSLASTSTKRVVAVGMAISGRV 145
Db      154 KIFSR-LIYIAQSGAMILTGTHGLTKYIGEVVRNTI--SRSEENIYVAIGIAMGMV 211
Qy      146 LHRRL--EAQDFPVNHPEDDGGSGQLCSIDNSHFLVEPFGPKGDLTELRL 202
Db      212 SNRDTLLRNCAEGEFLAQYIMDD--FTRDPLVILDNHNTHLILDVNGCHGHPTEAKLRN 270
Qy      203 RLEKHISE--ORAGYGTGSIETPVLCVLVNGDNTLERISRAVEQAAPMLILVSGGI 259
Db      271 QLEKHISERTTODSNYGG---KIPVCPAOGGKETLKAINTSIKKIPCVVVEGSGRI 326
Qy      260 ADVLAALVNQPHLLVPKVAEKQFKEKPPS--KHFSMEDIVRWTKLQNTSHOHLITYYD 317
Db      327 ADVIASLVEEDAPTSSAVKEKLVRLPRVTSRLESEETESWIKMLKEILCSHLITVYIK 386
Qy      318 FEQSGSELDVTIILKALVKACKSHSQEPQDYLDLKLAVANDRVIAKSEIFNGDVEWKS 377
Db      387 MEEAGDEIVSNAISYALYKAFSTSEQDKNNNGQLKLLBNQDLANDEIFTNDRWES 446
Qy      378 CDLEEVWDAVLSNKEPFRVLPVNDGADVADPLTYGLOELVRSKSLFDLQ--R 434
Db      447 ADLQEVMTALIKRPFVRLFLENGLNRKFLTHDVLTELF--SNHSTVLVRYMLQIAKN 505
Qy      435 KOEBAFLTLAGTQOAREPPAPRPAFSLHEVSRLKDFLODACGFQDGRPG--DRRA 493
Db      506 SYNDALLTF-----VKLVANFR---RGRKEDRNGRDEMID 539
Qy      494 EKGPAKPTGQKWLIDLNQKSENPWRDLFLMAVLONRHENATYFWAMQOEGVAAALACK 553
Db      540 E-----LHDVSPITRHPLOALFIWAILONKKELSKVIMEQTRGCTLAALGASK 587
Qy      554 ILKEMSHLETAEAARATREA--KYERLADLFSCYCSNSBARFALLVRRNRCKSTTC 611
Db      588 LKTLKAVKNDINAAGESEELANEYETRAVELFTECYSDEDLAEQLLVYSCAMGSGNC 647
Qy      612 LHLATEADAKAFPAHDVQAFLTRIMGDMAGPILRLGALCFALVYTNLTFSSEA 671
Db      648 LELAVEATDQHTAQOPGVQNLFSKOMYGEISRTQKMKIILCFIPLVGGFVSFRKK- 706
Qy      672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRPAVFLTLTRMKFWGAP 731
Db      707 -----PVDKHKK-----LMWYVVAFTTSP 725

```

QY 732 VTVEFGNVMYFAFLFTYVLLVDFRPPQSGSEVTLVFWVTLVEBIRGFFTDE 791
 DB 726 FVFSNMVVFYIAFLFLRAVLLMDFHVPH---PPELVLSLVVLFCDEVRQYVNGV 782
 QY 792 DTHLVKFFTLVVGDMNKCDAVAIFLFTVGTCRM---LPSAFAGRVTLAMDENVFTLR 848
 DB 783 N-----YFTDLMNWDTLGLFYFIAGIIVFRLHSSNKSLSYGRVIFCLDYIIFTLR 833
 QY 849 LHIHTAIHKQUGPKIIVVERMKKDVFFFLFSLVLAAGVTTQALLPHDGRLEWIRRR 908
 DB 834 LIHIFTVRNIGPKIIMQRMIDIVFFFLFAVMVAVGVARQOILRNEGRMWMIFRS 893
 QY 909 VLYRPLYOIFGOIPLDEIDEAR---VNCS-----THPLLE--DSPSCSLVYANMLVILL 959
 DB 894 VLYRPLYLAFGOVPSD--VDGTTYDPAHCTFTGNESKPLCVELDENHLP--PEWITPIV 951
 QY 960 VTFFLLVTVLMLNLLIAMESYTFVOVGNATMFKFORYNLIVEYHERPALAPPELLSH 1019
 DB 952 CIYMLSTNILLVNLVAMFGYVGVQENNDQVMKFORFLVQVCSRLNIPFPIVAFY 1011
 QY 1020 LSLTRRVFKKAHKEHLEHLEDPDPLDQKVVTMETVQKENFLSKMEKRRDSEGEVLR 1079
 DB 1012 FYMVVKKCFKCCCKEKNNESSVCCFKNEBNETLAMEGWKENYLVKINTKANDT--SEEMR 1070
 QY 1080 KTAHVDPLAKYLG--LRQEKRIK 1103
 DB 1071 HRFRODPTKANDLKGLEIKANKIK 1095

RESULT 15

US-09-895-793-778
 ; Sequence 778, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Reiter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Basols, Carlot
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.534C2
 ; CURRENT APPLICATION NUMBER: US/09/895,793
 ; NUMBER OF SEQ ID NOS: 982
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 778
 ; LENGTH: 1095
 ; TYPE: PR
 ; ORGANISM: Homo sapiens
 ; US-09-895-793-778

Query Match 25.7%; Score 1562.5; DB 10; Length 1095;
 Best Local Similarity 34.2%; Pred. No. 1.8e-135;
 Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

QY 26 GEVNFSGSKRGKFRVPSGAVSLPDLLEAEHMLPAPNLVSLVGEOPFAMKSWLR 85
 DB 95 GDIQFETIGKK--GKIRLSCTDDEILYELLTQMHMLKPTPLVSVTCGAGNFKLPRMR 153
 QY 86 DVLKRGVKAQAOSTGAMITLSALBVLGARHVGQAVRDSLASTSTKRVAVGASLCRV 145
 DB 154 KIFSR-LIYIQAOSKAWILTGTHYGLTKYGEVVRDWTI--SRSEENIIVAIIGIAAMGV 211
 QY 146 LHRRLLE---EAQDFFPHYEDDGGSGGCLSDNSHSHLIVEPRGPGGDLTEURL 202
 DB 212 SNRDTLRNCDAEGVFLAQYLMDD--FTRDPLIYILDNNTHLLVDNGCHGHPTEAKLRN 270
 QY 203 RLEKHISE---ORAGYGGTSGISEIPVLCILVNGDPNTERISRRAVEQAPMLILVSGSGI 259
 DB 271 QLEKHISRTIODSYGG---KPIYVCFAGGGETIKALINTSIKKNIPCVVSGSRI 326
 QY 260 ADVLAALVNOPLLVPKVAEKQFEKFPSS--KHFSWEDIIVWTKLQNTSHQHLITYD 317
 DB 327 ADVIASLVEVDAPTSAAVKEKLVRFPRVTSRLSEETESMIKWLKEILCSHLLTVIK 386
 QY 318 FEQGSSEELDTVILKALVKACKSHSQEPQDYLDLKLAVANDRVDIASEIFNGVEMKS 377
 DB 387 MEEAGDEIVSNAISYALYKASTSEODDNWNGOLKLENNQDLANDLFTNDRWES 446
 QY 378 CDLEEVWDALVSNKFEFVRLFVNDGADVADFLTYGRLOEYRSVRSKSLFDDLQ---R 434
 DB 447 ADLQEVMTALIKDRPKFVRLFLENGLNRKFLTHDUTLELF--SHFSTLYVRNIQIAKN 505
 QY 435 KOEBARLTLAGLGTQOAREPPAGPAPFSLHEVSVLKDFLODACGFYODGRPG--DRRA 493
 DB 506 SYNDALLTF-----VWKLVANFR---RGFKREDNRGDEMDI 539
 QY 494 EKGPARKPTGQKMLDLNOKSENPRDLFLAVVONRHEMATYFAMQOEGVAAALAAK 553
 DB 540 E-----LHDVSPITRHPLOALFIMAILONKKELSVWEQTRGCTLAALGASK 587
 QY 554 ILKESHLETEAARATREA--KYERLALDIFSECSYNSSEARFALLVRRNRCSKTYC 611
 DB 588 LKTLAKKNDIMNAGESEBELANETRAYELFTCTCYSDEDLAQOLLVSGEAMGSGNC 647
 QY 612 LHLATEADAKFAHADGVOAFLTRIMWGDMAAGPILRLGALFCALVYTNLTFSEBA 671
 DB 648 LELAVEATDQFTPAQPVQNFSLSKOWGEISBDTGMKIIILCFIPLVGCFSVFRKK- 706
 QY 672 PLRTGLEDLDLSDITREKSPLYGLQSRVEBELVEPRAGDGRPAVLLTRMRKMGAP 731
 DB 707 -----PVDKKKK-----LWYVAFFTSP 725
 QY 732 VTVEFGNVMYFAFLFTYVLLVDFRPPQSGSEVTLVFWVTLVEBIRGFFTDE 791
 DB 726 FVFSNMVVFYIAFLFLRAVLLMDFHVPH---PPELVLSLVVLFCDEVRQYVNGV 782
 QY 792 DTHLVKFFTLVVGDMNKCDAVAIFLFTVGTCRM---LPSAFAGRVTLAMDENVFTLR 848
 DB 783 N-----YFTDLMNWDTLGLFYFIAGIIVFRLHSSNKSLSYGRVIFCLDYIIFTLR 833
 QY 849 LHIHTAIHKQUGPKIIVVERMKKDVFFFLFSLVLAAGVTTQALLPHDGRLEWIRRR 908
 DB 834 LIHIFTVRNIGPKIIMQRMIDIVFFFLFAVMVAVGVARQOILRNEGRMWMIFRS 893
 QY 909 VLYRPLYOIFGOIPLDEIDEAR---VNCS-----THPLLE--DSPSCSLVYANMLVILL 959
 DB 894 VLYRPLYLAFGOVPSD--VDGTTYDPAHCTFTGNESKPLCVELDENHLP--PEWITPIV 951
 QY 960 VTFFLLVTVLMLNLLIAMESYTFVOVGNATMFKFORYNLIVEYHERPALAPPELLSH 1019
 DB 952 CIYMLSTNILLVNLVAMFGYVGVQENNDQVMKFORFLVQVCSRLNIPFPIVAFY 1011
 QY 1020 LSLTRRVFKKAHKEHLEHLEDPDPLDQKVVTMETVQKENFLSKMEKRRDSEGEVLR 1079
 DB 1012 FYMVVKKCFKCCCKEKNNESSVCCFKNEBNETLAMEGWKENYLVKINTKANDT--SEEMR 1070

Wed Sep 10 09:59:28 2003

us-09-834-792c-4.rapb

Page 13

Qy 1080 KTAHRVDFIAKYLGG-LRQOEKRIK 1103
::|||::||
Db 1071 HRFRLDTKLNLDLKGILKEIANIK 1095

Search completed: September 10, 2003, 09:47:00
Job time : 37 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2003, 09:30:34 ; Search time 46 Seconds
(without alignments)
6535.463 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6031
Sequence: 1 MODVGGPRPGSGDAEDRRR.....HRGGIDGWEQPGAGQPSDRT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6073	99.7	1165	4 Q9NZQ8	Q9NZQ8 homo sapien
2	6019	98.8	1159	4 Q9NY34	Q9NY34 homo sapien
3	5068.5	83.2	1158	11 Q9JUH7	Q9JUH7 mus musculus
4	5018.5	82.4	1148	11 Q9EPM4	Q9EPM4 mus musculus
5	5008.5	82.2	1148	11 Q9NPF9	Q9NPF9 mus musculus
6	4963.5	81.5	1116	11 Q9EPM3	Q9EPM3 mus musculus
7	4445.5	73.0	1030	11 Q9BS44	Q9BS44 mus musculus
8	2430.5	33.9	1214	4 Q8TD43	Q8TD43 homo sapien
9	2166.5	35.6	1040	4 Q9GL84	Q9GL84 homo sapien
10	2146	35.2	1016	4 Q9NXXV1	Q9NXXV1 mus musculus
11	2051	33.7	945	11 Q8BLM7	Q8BLM7 mus musculus
12	2024	33.2	1507	11 Q91YD4	Q91YD4 mus musculus
13	1578	25.9	1104	11 Q8RAD5	Q8RAD5 mus musculus
14	1563.5	25.7	1104	11 Q8RAD5	Q8RAD5 mus musculus
15	1559.5	25.6	1095	4 Q8TDX8	Q8TDX8 homo sapien
16	1559.5	25.6	1104	4 Q8TAC3	Q8TAC3 homo sapien

17	1228.5	20.2	1533	4 Q75560	Q75560 homo sapien
18	1208.5	19.8	1862	11 Q925B2	Q925B2 mus musculus
19	1208.5	19.8	1863	11 Q923J1	Q923J1 mus musculus
20	1208.5	19.8	1863	11 Q9JLQ1	Q9JLQ1 mus musculus
21	1183.5	19.4	1864	4 Q9BX82	Q9BX82 homo sapien
22	1183.5	19.4	1865	4 Q9BQT4	Q9BQT4 homo sapien
23	1174.5	19.3	2022	4 Q9BX84	Q9BX84 homo sapien
24	1157	19.0	2028	11 Q8CIR4	Q8CIR4 mus musculus
25	1141	18.7	1131	5 Q9V7A5	Q9V7A5 dirosophila
26	1139.5	18.7	686	6 Q8HXH2	Q8HXH2 macaca fasc
27	1113.5	18.3	485	11 Q9ES05	Q9ES05 rattus norv
28	1064	17.5	1971	5 Q8IG04	Q8IG04 caenorhabdi
29	1062	17.4	2032	5 Q93971	Q93971 caenorhabdi
30	1048	17.2	1078	5 Q8MLA4	Q8MLA4 dirosophila
31	990	16.3	1363	5 Q20766	Q20766 caenorhabdi
32	887.5	14.6	1681	5 Q8IG05	Q8IG05 caenorhabdi
33	881	14.5	1707	5 Q17652	Q17652 caenorhabdi
34	874.5	14.4	1133	4 Q9H637	Q9H637 homo sapien
35	863	14.2	848	11 Q8BIH6	Q8BIH6 mus musculus
36	818	13.4	1122	5 Q8IG06	Q8IG06 caenorhabdi
37	687.5	11.3	737	11 Q8BJ11	Q8BJ11 mus musculus
38	593	9.7	515	11 Q8C787	Q8C787 mus musculus
39	564	9.3	575	4 Q9HXQ2	Q9HXQ2 homo sapien
40	498	8.2	542	11 Q703J4	Q703J4 mus musculus
41	458.5	7.5	640	6 Q9GMW4	Q9GMW4 macaca fasc
42	360	5.9	372	11 Q9CUT2	Q9CUT2 mus musculus
43	349	5.7	338	4 Q9H200	Q9H200 homo sapien
44	341.5	5.6	361	11 Q8BI66	Q8BI66 mus musculus
45	341.5	5.6	369	11 Q8BK11	Q8BK11 mus musculus

ALIGNMENTS

RESULT 1

Q9NZQ8 PRELIMINARY; PRT; 1165 AA.
AC Q9NZQ8;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE MTR1.
GN MTR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20076317; PubMed=10607831;
RA Pravit D., Enklar T., Klemm G., Gaertner B., Spangenberg C.,
RT Wierpach A., Higgins M., Pelletier J., Zabel B.,
RT "Identification and characterization of MTR1, a novel gene with
RT homology to melastatin (MLSN1) and the tip gene family located in the
RT BMS-WT2 critical region on chromosome 11p15.5 and showing allele-
RT specific expression."
RT Hum. Mol. Genet. 9:203-216(2000).
RL Hum. Mol. Genet. 9:203-216(2000).
DR EMBL; AF174473; AAF26288.1; --
DR GenBank; HGNC:14323; TRPM5.
DR InterPro; IPR002111; Cat_channel_Trl.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans. 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1165 AA; 131450 MW; C4AD5BAA866BE73B CRC64;

Query Match

Best Local Similarity 99.7%; Score 6073; DB 4; Length 1165;
Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MODVGGPRPGSGDAEDRRRLGLHGEVNFPGSGKKRKFPVRVPGVAPSVLFDLLLEW 60
DB 1 MODVGGPRPGSGDAEDRRRLGLHGEVNFPGSGKKRKFPVRVPGVAPSVLFDLLLEW 60

```

QY 61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVGLARHVQAV 120
QY 121 RHSLASTSTKRVVAVGMAISGRVLRHRIIEBAQEDPVVHYPEDDGSQGLCSLDSVL 180
DB 121 RHSLASTSTKRVVAVGMAISGRVLRHRIIEBAQEDPVVHYPEDDGSQGLCSLDSVL 180
QY 181 SHPILVEPPGPKDGLTELRLRLKHSISEORAGYGGTSSIEIPVLCILVNDPNTLERI 240
DB 181 SHPILVEPPGPKDGLTELRLRLKHSISEORAGYGGTSSIEIPVLCILVNDPNTLERI 240
QY 241 SRAVEQAPMILVSGSGIADVLALVNPRLVPEKVAEKORKEKPPSKHFSWEDIVRWT 300
DB 241 SRAVEQAPMILVSGSGIADVLALVNPRLVPEKVAEKORKEKPPSKHFSWEDIVRWT 300
QY 301 KLLQNTSHQHLLTYVDFEQSGSEELDTYILKALVKAQSHQEPDODYIDELKLVAMDR 360
DB 301 KLLQNTSHQHLLTYVDFEQSGSEELDTYILKALVKAQSHQEPDODYIDELKLVAMDR 360
QY 361 VIAKSEIPNGDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVDLTYGRLQELVR 420
DB 361 VIAKSEIPNGDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVDLTYGRLQELVR 420
QY 421 SVSRKSLJFDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSRVLKDLQDADCRG 480
DB 421 SVSRKSLJFDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSRVLKDLQDADCRG 480
QY 481 PVOQGRPGDRRRAEKAPRAKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAITYFMAM 540
DB 481 PVOQGRPGDRRRAEKAPRAKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAITYFMAM 540
QY 541 GQEGVAAALAAKIIKEMSHLETEBAARATREAKERLALPFSCEVNSBARAFALLV 600
DB 541 GQEGVAAALAAKIIKEMSHLETEBAARATREAKERLALPFSCEVNSBARAFALLV 600
QY 601 RNRNCSKTTCHLATEADAKAFPAHDVQAFLTRIMWDMAGTPILRLGAPLCPALV 660
DB 601 RNRNCSKTTCHLATEADAKAFPAHDVQAFLTRIMWDMAGTPILRLGAPLCPALV 660
QY 661 YNNLITTFSEAPLRGLLEDLQDLSDLTBKSPLYGLQSRVEELVEAPRAQGRGRAVFL 720
DB 661 YNNLITTFSEAPLRGLLEDLQDLSDLTBKSPLYGLQSRVEELVEAPRAQGRGRAVFL 720
QY 721 LTRMRKPMGAPVTVFIGNVVMYFALFLPTVYLVLDPRPPQSGSPBEVTLTFWFTLV 780
DB 721 LTRMRKPMGAPVTVFIGNVVMYFALFLPTVYLVLDPRPPQSGSPBEVTLTFWFTLV 780
QY 781 BEIRQGFPTDEDTLHVKFTLLYVGNMNCMDVAFILFIVGTCTMLPSAFEAQRTVLAM 840
DB 781 BEIRQGFPTDEDTLHVKFTLLYVGNMNCMDVAFILFIVGTCTMLPSAFEAQRTVLAM 840
QY 841 DPMVETLRLIHFALHKOIGPKIIVERMMKOVFFFLPFLSVMLVAYGTTQALLHPHDG 900
DB 841 DPMVETLRLIHFALHKOIGPKIIVERMMKOVFFFLPFLSVMLVAYGTTQALLHPHDG 900
QY 901 RLEWIFRRRLYRPLYOIFGOIPLDEIDEARVNCSTPILLEDSPSCPSLYAMWLITLLV 960
DB 901 RLEWIFRRRLYRPLYOIFGOIPLDEIDEARVNCSTPILLEDSPSCPSLYAMWLITLLV 960
QY 961 TELVLTNNVLNMLLAMPSTYFOVQGNATWEMKFORVNLIVEYHERPALAPFILLSTL 1020
DB 961 TELVLTNNVLNMLLAMPSTYFOVQGNATWEMKFORVNLIVEYHERPALAPFILLSTL 1020
QY 1021 SLTLRRVFEKKEAEHREHLERDLPDLQKVTWTWQENFLSYMEKRRDSEGBVLARK 1080
DB 1021 SLTLRRVFEKKEAEHREHLERDLPDLQKVTWTWQENFLSYMEKRRDSEGBVLARK 1080
QY 1081 TAAHVDLFAKLYGSLREOEKRIKCLSEQINVCSSVSSVADVLACGGGRSSOHGEGSQ 1140
DB 1081 TAAHVDLFAKLYGSLREOEKRIKCLSEQINVCSSVSSVADVLACGGGRSSOHGEGSQ 1140
QY 1141 LVAADHRGGLDGEOPGAGQPPSDT 1165

```

```

DB 1141 LVAADHRGGLDGEOPGAGQPPSDT 1165
RESULT 2
AC Q9NY34 PRELIMINARY; PRT: 1159 AA.
ID Q9NY34;
AD Q9NY34;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE LTRPC5 protein (Fragment).
GN LTRPC5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Paulsen M., El-Maari O., Engemann S., Franck O., Stroedicke M.,
RA Davies K.R., Bowden L.M., Reinhardt R., Reik W., Harteneck C.,
RA Walter J.;
RT "Comparative sequence analysis and characterization of the imprinting
RT cluster on the human chromosome 11p15.5 and distal mouse chromosome
RT 7."
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ270996; CAB6342.1; -.
DR InterPro: IPR002111; Cat_channel_TripL.
DR InterPro: IPR005821; Ion_trans.
DR Pfam: PF00520; Ion_trans.
DR Ionic channel; Transmembrane.
FT NON-TER
SQ SEQUENCE 1159 AA; 130775 MW; E31658C1125363B CRC64;
Query Match 98.8%; Score 6019; DB 4; Length 1159;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1154; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 9 PSQPDADRRBELGLHGEVNFVGGGKRGKGFVRPVSVAAPSVLFDLLAEHMLPAPMLV 68
DB 9 PSQPDADRRBELGLHGEVNFVGGGKRGKGFVRPVSVAAPSVLFDLLAEHMLPAPMLV 68
QY 1 VSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVGLARHVQAVRHSLAST 128
DB 1 VSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVGLARHVQAVRHSLAST 128
QY 61 VSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVGLARHVQAVRHSLAST 120
DB 61 VSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVGLARHVQAVRHSLAST 120
QY 129 STKRVVAVGMAISGRVLRHRIIEBAQ--EDPPHYPPEDDGSQGLCSLDSNLSHPLV 186
DB 129 STKRVVAVGMAISGRVLRHRIIEBAQ--EDPPHYPPEDDGSQGLCSLDSNLSHPLV 186
QY 121 STKRVVAVGMAISGRVLRHRIIEBAQVHEDFPVHYPEDDGSQGLCSLDSNLSHPLV 180
DB 121 STKRVVAVGMAISGRVLRHRIIEBAQVHEDFPVHYPEDDGSQGLCSLDSNLSHPLV 180
QY 187 EPGPPGKGDGTELRLRLKHSISEORAGYGGTSSIEIPVLCILVNDPNTLERISRAVEQ 246
DB 187 EPGPPGKGDGTELRLRLKHSISEORAGYGGTSSIEIPVLCILVNDPNTLERISRAVEQ 246
QY 241 AAPMLILVSGSGIADVLALVNPRLVPEKVAEKORKEKPPSKHFSWEDIVRMTKLONI 306
DB 241 AAPMLILVSGSGIADVLALVNPRLVPEKVAEKORKEKPPSKHFSWEDIVRMTKLONI 306
QY 307 TSHQHLTVYPPFEGSGSELDVTYILKALVKAQSHQEPDODYIDELKLVAMDRVDIAKS 366
DB 307 TSHQHLTVYPPFEGSGSELDVTYILKALVKAQSHQEPDODYIDELKLVAMDRVDIAKS 366
QY 301 TSHQHLTVYPPFEGSGSELDVTYILKALVKAQSHQEPDODYIDELKLVAMDRVDIAKS 360
DB 301 TSHQHLTVYPPFEGSGSELDVTYILKALVKAQSHQEPDODYIDELKLVAMDRVDIAKS 360
QY 367 EIPNGDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVDLTYGRLQELVRSVSRKS 426
DB 367 EIPNGDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVDLTYGRLQELVRSVSRKS 426
QY 427 LTFDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSRVLKDLQDADCRGFDYODGR 486
DB 427 LTFDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSRVLKDLQDADCRGFDYODGR 486
QY 487 PGRRRRAEKAPRAKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAITYFMAMQOEGVA 546
DB 487 PGRRRRAEKAPRAKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAITYFMAMQOEGVA 546

```



```

QY 547 AALAACTLKEMSHLSEAEARATREAKYERLALDLFSECCYSNSEARAFALLVRRNCW 606
Db 541 AALAACTLKEMSHLSEAEARATREAKYERLALDLFSECCYSNSEARAFALLVRRNCW 600
QY 607 SKTCTLHATENDADAFPAHDGVQAFLTRIMWGDMAAGTPIRLILGAFICPLVYTNLIT 666
Db 601 SKTCTLHATENDADAFPAHDGVQAFLTRIMWGDMAAGTPIRLILGAFICPLVYTNLIT 660
QY 667 FSEAPLRTGLEDDLODLSLDTKEKSPYLQSGRVEELVEAPRAQDGRGPAFELLTRMK 726
Db 661 FSEAPLRTGLEDDLODLSLDTKEKSPYLQSGRVEELVEAPRAQDGRGPAFELLTRMK 720
QY 727 FWGAPVTVFLGNVWYFAFLFLFTVLLVDPRPPQSGSGPEVTLVFWFTLVLEIRIG 786
Db 721 FWGAPVTVFLGNVWYFAFLFLFTVLLVDPRPPQSGSGPEVTLVFWFTLVLEIRIG 780
QY 787 FTTDEDTLHVKKFTLYVGDNNKCMVAIFLFTVGTCTMLPSAEAGRTVLAMDPMVFT 846
Db 781 FTTDEDTLHVKKFTLYVGDNNKCMVAIFLFTVGTCTMLPSAEAGRTVLAMDPMVFT 840
QY 847 LRLHIFAIHKQAGPKIIVERRMKDVFPEFLFSLVWLVAAGVTQALLHPHDSLEWIF 906
Db 841 LRLHIFAIHKQAGPKIIVERRMKDVFPEFLFSLVWLVAAGVTQALLHPHDSLEWIF 900
QY 907 RRVLYRPLYQIFGQIPLDEIDEARVNCSTHPLLEDSPSCSLYANMLVILLVTFLLVT 966
Db 901 RRVLYRPLYQIFGQIPLDEIDEARVNCSTHPLLEDSPSCSLYANMLVILLVTFLLVT 960
QY 967 NVLLMNLIIAMFSYFOYVQGNATPMKFORYNLIVETHERPALAPPTILSHSLTLRR 1026
Db 961 NVLLMNLIIAMFSYFOYVQGNATPMKFORYNLIVETHERPALAPPTILSHSLTLRR 1020
QY 1027 VFKEAEKREHLERDLDPDOKVYVETVQKFNFLSKMEKRSPDSGEVLRKTAHVD 1086
Db 1021 VFKEAEKREHLERDLDPDOKVYVETVQKFNFLSKMEKRSPDSGEVLRKTAHVD 1080
QY 1087 FIAKTLGLRBOEKIKCLESQINYSVLVSSVADVLAAQGGPRSSQHCGESQCLVAADH 1146
Db 1081 FIAKTLGLRBOEKIKCLESQINYSVLVSSVADVLAAQGGPRSSQHCGESQCLVAADH 1140
QY 1147 RGGIDGWEQPGAGPPSDT 1165
Db 1141 RGGIDGWEQPGAGPPSDT 1159

RESULT 3
Q9JUH7 PRELIMINARY; PRT; 1158 AA.
ID Q9JUH7
AC Q9JUH7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE MSLN1-and TRP-related protein 1 (MTR1).
DE TRPM5 OR LTRP5 OR MTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10907850;
RA Yatsuki H., Watanabe H., Hattori M., Joh K., Soejima H., Komoda H.,
RA Xin Z., Zhu X., Higashimoto K., Nishimura M., Kuratomi S., Sasaki H.,
RA Sasaki Y., Maki T.;
RT "Sequence-based structural features between Kv1q1 and Tapal on mouse
RT chromosome 7q4/7s corresponding to the Beckwith-Wiedemann syndrome
RT intronic sequences of Kv1q1 between mouse and human.";
RL DNA Res. 7:195-206(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2036135; PubMed=10903843;

```

```

RA Enkelaar T., Esswein M., Oswald M., Hilbert K., Winterpacht A.,
RA Higgins M., Zabel B., Prawitt D.;
RT "Mtr1, a Novel Allelically Expressed Gene in the Center of the Mouse
RT Distal Chromosome 7 Imprinting Cluster, is a Member of the Trp Gene
RT Family.";
RL Genomics 67:179-187(2000).
DR EMBL; AB039952; BAA96877.1; -
DR EMBL; AF228681; AAF98120.1; -
DR MGD; MGI:1861718; Trpm5.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KM Ionc Channel; Transmembrane.
SQ SEQUENCE 1158 AA; 130843 MW; FOA5237EC67867CE CRC64;

Query Match 83.2%; Score 5068.5; DB 11; Length 1158;
Beet Local Similarity 83.9%; Pred. No. 0;
Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

QY 1 MODVQPPGSPGDAEDRRELGLHGEVNFSGSGKGGKGFYRVPBGVAPSVLFDLLAEW 60
Db 1 MOTTQSSGSGSPPTDECMEPILCRGEINFGSGSKGKGFYKVPSSVAPSVLFDLLAEW 60
QY 61 HLPAPNLVSLVGEERPLAMKSWLRDYLKGLVKAAGTGAMILTSALVGLARRVQAV 120
Db 61 HLPAPNLVSLVGEERPLAMKSWLRDYLKGLVKAAGTGAMILTSALVGLARRVQAV 120
QY 121 RDHSLASTSTVRRVAVAGMAGLGVLRRLILE--EAQEDFVHVPEDDGSQPLCSIDS 178
Db 121 RDHSLASTSTIRVVAIGMAGSLDRIILHRLQLDGVHOKDPTIHPADGNIQGPLCPIDS 180
QY 179 NLSHFIIIVPEPPPKG--DGLTELRLLEKHSIEQAGVGSGSIEIPVLCILVNGDPTL 237
Db 181 NLSHFIIIVSALSSGNDGLTELDSLEKHSIQORTGCGTSCIQIPVLCILVNGDPTL 240
QY 238 ERISRAVEQAAPWILVSGGSIADVLAALVQNPHLVLPKVAEKQFEKFPKHSWEDIV 297
Db 241 ERISRAVEQAAPWILVSGGSIADVLAALVQNPHLVLPKVAEKQFEKFPKHSWEDIV 300
QY 298 RWTLLQNTHTSHQHLTYRDEQSGSELDVITIKALVYKAKSHSQEODYLDLKLAVA 357
Db 301 HTTELQNTIAHPHLTYRDEQSGSELDVITIKALVYKAKSHSQEODYLDLKLAVA 360
QY 358 WDRVDIAKSEIFNGDVWKSCDLEWVWDALVSNKPEFVRFLVNGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSEIFNGDVWKSCDLEWVWDALVSNKPEFVRFLVNGADVADFLTYGRLOE 420
QY 418 LYSVSRKSLFDLLQKOEERLTLAAGTQARBPAPASLHESRVLXDLODA 477
Db 421 LYSVSRKSLFDLLQKOEERLTLAAGTQARBPAPASLHESRVLXDLODA 480
QY 478 CRGYQDGRPEDRRRAEKPAKRTQGWKILDLNOKSENPVRDILPLVAVLONRHMATYF 537
Db 481 CRGYQDGR---RMEERGPKPRAQCKWLPDLRSKSEDPDRDLFLVAVLONRYEMATYF 536
QY 538 WAMGQGVAAALAACTLKEMSHLSEAEARATREAKYERLALDLFSECCYSNSEARAF 597
Db 537 WAMGQGVAAALAACTLKEMSHLSEAEARATREAKYERLALDLFSECCYSNSEARAF 596
QY 598 LTVRRNCSKTTCTLHATENDADAKAFPAHDGVQAFLTRIMWGDMAAGTPIRLILGAFICF 657
Db 597 LTVRRNCSKTTCTLHATENDADAKAFPAHDGVQAFLTRIMWGDMAAGTPIRLILGAFICF 656
QY 658 ALVYTNLITPSEAPLRTGLEDDLODLSLDTKEKSPYLQSGRVEELVEAPRAQDGRGPA 717
Db 657 ALVYTNLITPSEAPLRTGLEDDLODLSLDTKEKSPYLQSGRVEELVEAPRAQDGRGPA 716
QY 718 VFLLTRRKFWGAVTVFLGNVWYFAFLFLFTVLLVDPRPPQSGSGPEVTLVFWFT 777
Db 717 VFLLTRRKFWGAVTVFLGNVWYFAFLFLFTVLLVDPRPPQSGSGPEVTLVFWFT 776
QY 778 LVLEIRIQGFTDEDTLHVKKFTLYVGDNNKCMVAIFLFTVGTCTMLPSAEAGRTV 837

```

```

Db 777 LVLEIRGQFPTDEDTLHVKKFTLVYEDNMNKCMDVAIFLIVGTTCMVBSVFAGRTV 836
Qy 838 LAMDMVTTLRILHFAHKKOLGPKIIVERMKVFFFLFSLVWLVAYGTTTALLHP 897
Db 837 LAIDMVFTRLRILHFAHKKOLGPKIIVERMKVFFFLFSLVWLVAYGTTTALLHP 896
Qy 898 HDGRLEWIFRRVLVYPIQIFQIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 957
Db 897 HDGRLEWIFRRVLVYPIQIFQIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 956
Qy 958 LVLFTLVNTVNLMLLJAMFSYTFQVYQGNATMFKQRYNLIVEYHERPALAPFILL 1017
Db 957 LVLFTLVNTVNLMLLJAMFSYTFQVYQGNATMFKQRYNLIVEYHERPALAPFILL 1016
Qy 1018 SHLSLTLRVFKKEHKEHREHLRDLPPDLQKVTWETVQENFLSKMEKRRRDEGEV 1077
Db 1017 SHLSLTLRVFKKEHKEHREHLRDLPPDLQKVTWETVQENFLSKMEKRRRDEGEV 1076
Qy 1078 LKRTAHRVDLAKYIGGLREGEKRIKCLSEQINYSVLVSVADYLAQGGPRSSQHCSE 1137
Db 1077 LKRTAHRVDLAKYIGGLREGEKRIKCLSEQINYSVLVSVADYLAQGGPRSSQHCSE 1136
Qy 1138 GSQLVADHRRGIDGMEQPGACQPPSDT 1165
Db 1137 RSQPASARDR-----EYLESGLPPSDT 1158

```

RESULT 4

```

Q9EBM4 PRELIMINARY; PRT; 1148 AA.
ID Q9EBM4 AC Q9EBM4:
AC Q9EBM4:
DB 01-MAR-2001 (TREMBLrel. 16, Created)
DB 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DB 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE ltrpc5 protein.
GN TRPM5 OR ltrpc5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX MEDLINE=20377495; PubMed=10915772;
RA Paulsen M., El-Maari O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RA "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RT Hum. Mol. Genet. 9:1829-1841(2000).
DR EMBL; AJ251835; CAC19456.1; -
DR MGD; MGI:1861718; Trpm5.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans.1.
KM Ionic channel; Transmembrane.
SQ SEQUENCE 1148 AA; 129630 MW; 947AF5B9CFDCA127 CRC64;

```

```

Query Match 82.4%; Score 5018.5; DB 11; Length 1148;
Best Local Similarity 85.3%; Pred. No. 0;
Matches 964; Conservative 63; Mismatches 96; Indels 7; Gaps 3;

```

```

Qy 1 MODVCGPRGSGDADRELGLHGEVNVFGSGKKRGKRVNVPASVAFDILLAEW 60
Db 1 MOTTGSSCGSPEDTDEGWEPLICRGEINFGSGKKRGKRVNVPASVAFDILLAEW 60
Qy 61 HLPAPLVVSLVGEBOFPAMKSWLRDVLKRGKLVKAAQSTGAMLTLSALRGVLAHVQAV 120
Db 61 HLPAPLVVSLVGEBOFPAMKSWLRDVLKRGKLVKAAQSTGAMLTLSALRGVLAHVQAV 120
Qy 121 RDHSLASTSTKRVVAVNAGSLGRVLHRRILE--EAQEDFPVHYPEDGSGQGLCPLSDS 178
Db 121 RDHSLASTSTKRVVAVNAGSLGRVLHRRILE--EAQEDFPVHYPEDGSGQGLCPLSDS 178
Qy 121 RDHSLASTSTKRVVAVNAGSLGRVLHRRILE--EAQEDFPVHYPEDGSGQGLCPLSDS 180
Db 121 RDHSLASTSTKRVVAVNAGSLGRVLHRRILE--EAQEDFPVHYPEDGSGQGLCPLSDS 180

```

```

Qy 179 NLSHFILVEPGPPGKG-DGLTELRRLREKHISEORAGYGTGSIPIVLCLLVNGDPNTL 237
Db 181 NLSHFILVEPGALSGNDGLTELQSLSEKHSIQGRGTGSGTSCIQIPVCLLVNGDPNTL 240
Qy 238 ERISRAVEQAAPMLILVSGGSIADYLAALVNQPHILVVKVAEKQFKKFPKSPHSEDIY 297
Db 241 ERISRAVEQAAPMLILVSGGSIADYLAALVNSQPHILVQVAKQFKREFPEECSEWAIY 300
Qy 298 RMTKLONITSHOHLITYYDEPGSGSELDIVIIKALVKAKCSHQEQPDYLDLKLVA 357
Db 301 HETLONITAAHPHILITYYDEPGSGSELDIVIIKALVKAKCSHQEQPDYLDLKLVA 360
Qy 358 WDRVDIAKSEIFNGDVEKSCDLEEVWVDAVSNKPEFVRFLVDNGADVADFLTYGRIOE 417
Db 361 WDRVDIAKSEIFNGDVEKSCDLEEVWVDAVSNKPEFVRFLVDNGADVADFLTYGRIOE 420
Qy 418 LYRSYRSKSLFDLLQKQSEARLTLAIGTQOARREPPAGSPASLHVSVLNDFLODA 477
Db 421 LYHSVSPKSLFELLQKQSEARLTLAIGTQOARELTLGAPSLHVSRLKDFLHDA 480
Qy 478 CRGFYQDGRPGDRRAEKGPAKRPFGQKMLDLNOKSENPMRDLFLMAVLONRHEMATYF 537
Db 481 CRGFYQDGRPGDRRAEKGPAKRPFGQKMLDLNOKSENPMRDLFLMAVLONRHEMATYF 536
Qy 538 WAMGQEGVAAALAAACKIILEKMSHLETEAARATREARYERLADLFSECYSNSERAPFA 597
Db 537 WAMGREGVAAALAAACKIILEKMSHLEKEABAVARTREARYEQLADLFSECYSNSERAPFA 596
Qy 598 LLVRRNRCSKTTCLHLATEADAKAFPHADGVQAFRTIWMGDMAAGTPIRLILGAPLCF 657
Db 597 LLVRRNRCSKTTCLHLATEADAKAFPHADGVQAFRTIWMGDMAAGTPIRLILGAPLCF 656
Qy 658 ALVYTNLTFSSEBAFLRTGLDLODLSDTEKPSLYGLOSREBELVAPRAQGRGPRA 717
Db 657 ALVYTNLTFSSEBAFLRTGLDLODLSDTEKPSLYGLOSREBELVAPRAQGRGPRA 716
Qy 718 VELLTRMRKFWGAPVTVFLGNVVMYFAFLFTYVVLVDPRPPGSPGSEVTVLYFWFT 777
Db 717 AFLTRMRKFWGAPVTVFLGNVVMYFAFLFTYVVLVDPRPPGSPGSEVTVLYFWFT 776
Qy 778 LVLEIRGQFPTDEDTLHVKKFTLVYGNMNCMDVAIFLIVGTTCMVBSVFAGRTV 837
Db 777 LVLEIRGQFPTDEDTLHVKKFTLVYEDNMNKCMDVAIFLIVGTTCMVBSVFAGRTV 836
Qy 838 LAMDMVTTLRILHFAHKKOLGPKIIVERMKVFFFLFSLVWLVAYGTTTALLHP 897
Db 837 LAIDMVFTRLRILHFAHKKOLGPKIIVERMKVFFFLFSLVWLVAYGTTTALLHP 896
Qy 898 HDGRLEWIFRRVLVYPIQIFQIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 957
Db 897 HDGRLEWIFRRVLVYPIQIFQIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 956
Qy 958 LVLFTLVNTVNLMLLJAMFSYTFQVYQGNATMFKQRYNLIVEYHERPALAPFILL 1017
Db 957 LVLFTLVNTVNLMLLJAMFSYTFQVYQGNATMFKQRYNLIVEYHERPALAPFILL 1016
Qy 1018 SHLSLTLRVFKKEHKEHREHLRDLPPDLQKVTWETVQENFLSKMEKRRRDEGEV 1077
Db 1017 SHLSLTLRVFKKEHKEHREHLRDLPPDLQKVTWETVQENFLSKMEKRRRDEGEV 1076
Qy 1078 LKRTAHRVDLAKYIGGLREGEKRIKCLSEQINYSVLVSVADYLAQGG 1127
Db 1077 LKRTAHRVDLAKYIGGLREGEKRIKCLSEQINYSVLVSVADYLAQGG 1126

```

RESULT 5

```

Q99NF9 PRELIMINARY; PRT; 1148 AA.
ID Q99NF9 AC Q99NF9:
AC Q99NF9:
DB 01-JUN-2001 (TREMBLrel. 17, Created)
DB 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DB 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE ltrpc5 protein.

```

GN TRPM5 OR LTRPC5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RA Stroedicke M.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RA MEDLINE=20377495; PubMed=10915772;
 RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
 RA Davies K., Reinhardt R., Reik W., Walter J.;
 RT "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RL Hum. Mol. Genet. 9:1829-1841(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RA Engemann S.;
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ271092; CAB94717.2; -.
 DR MGD; MGI:1861718; Trpm5.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_channel_TrpL.
 DR Pfam; PF00520; Ion_trans_1.
 KM Ionic channel; Transmembrane.
 SQ SEQUENCE 1148 AA; 82950 MW; 90517E8557DCA127 CRC64;
 Query Match 82.2%; Score 5008.5; DB 11; Length 1148;
 Best Local Similarity 85.2%; Pred. No. 0;
 Matches 963; Conservative 63; Mismatches 97; Indels 7; Gaps 3;
 QY 1 MOVVQGPSPGDAEDRELGLHGEVNFSGSGKRGKRVVPBGVAPSVLFDLLLAEW 60
 DB 1 MOTTQSCPGSPPTDEDMEPILCRGEINFGSGKRGKRVVPBGVAPSVLFDLLLAEW 60
 QY 61 HLPAPNLVSLVGEQPPAMKSLRDVLRKGLVRAOCTGAWILTSARVGLARVGVAV 120
 DB 61 HLPAPNLVSLVGEQPPAMKSLRDVLRKGLVRAOCTGAWILTSARVGLARVGVAV 120
 QY 121 RDHSLASTSTKYVAVAGMAGSLGRVLRILE--EAQEDFPVHYEDDDGSGPLCLSDS 178
 DB 121 RDHSLASTSTKYVAVAGMAGSLGRVLRILE--EAQEDFPVHYEDDDGSGPLCLSDS 178
 QY 121 RDHSLASTSTKYVAVAGMAGSLGRVLRILE--EAQEDFPVHYEDDDGSGPLCLSDS 180
 DB 121 RDHSLASTSTKYVAVAGMAGSLGRVLRILE--EAQEDFPVHYEDDDGSGPLCLSDS 180
 QY 179 NLSHFILVEGPPGKG-DGLTELRLLEKHSIQORAGYGTGSIPIVLCILVNGDPNTL 237
 DB 179 NLSHFILVEGPPGKG-DGLTELRLLEKHSIQORAGYGTGSIPIVLCILVNGDPNTL 237
 QY 181 NLSHFILVESGALSGNDGLTELQSLSEKHSIQORAGYGTGSIPIVLCILVNGDPNTL 240
 DB 181 NLSHFILVESGALSGNDGLTELQSLSEKHSIQORAGYGTGSIPIVLCILVNGDPNTL 240
 QY 238 ERIRAVEQAPWILLVSSGSIADVLALVNQPHLVKVAEKQPKKEFKSHSWEIV 297
 DB 238 ERIRAVEQAPWILLVSSGSIADVLALVNQPHLVKVAEKQPKKEFKSHSWEIV 297
 QY 241 ERIRAVEQAPWILLVSSGSIADVLALVNQPHLVKVAEKQPKKEFKSHSWEIV 300
 DB 241 ERIRAVEQAPWILLVSSGSIADVLALVNQPHLVKVAEKQPKKEFKSHSWEIV 300
 QY 298 RWTKLQNTSHQHLTYDFEFGSGSELDVTYIKALKVAKCKSHSQEODYLDLKLAVA 357
 DB 298 RWTKLQNTSHQHLTYDFEFGSGSELDVTYIKALKVAKCKSHSQEODYLDLKLAVA 357
 QY 301 HMTLQNLQIAHPHLTYDFEFGSGSELDVTYIKALKVAKCKSHSQEODYLDLKLAVA 360
 DB 301 HMTLQNLQIAHPHLTYDFEFGSGSELDVTYIKALKVAKCKSHSQEODYLDLKLAVA 360
 QY 358 WDRVDIAKSEIFNGDEVKSCDLEEVVADLVSNKPEFVRLFVNGADVADFLTYGRLOE 417
 DB 358 WDRVDIAKSEIFNGDEVKSCDLEEVVADLVSNKPEFVRLFVNGADVADFLTYGRLOE 417
 QY 361 WDRVDIAKSEIFNGDEVKSCDLEEVVADLVSNKPEFVRLFVNGADVADFLTYGRLOE 420
 DB 361 WDRVDIAKSEIFNGDEVKSCDLEEVVADLVSNKPEFVRLFVNGADVADFLTYGRLOE 420
 QY 418 LYRSVSRKSLFDLLQKQEBARLTLAGLGTQOARPPAPGAPPSLHVSVKLDPLQDA 477
 DB 418 LYRSVSRKSLFDLLQKQEBARLTLAGLGTQOARPPAPGAPPSLHVSVKLDPLQDA 477
 QY 421 LYHSVSPSSLLFELLQKQEBARLTLAGLGTQOARPPAPGAPPSLHVSVKLDPLQDA 480
 DB 421 LYHSVSPSSLLFELLQKQEBARLTLAGLGTQOARPPAPGAPPSLHVSVKLDPLQDA 480
 QY 478 CRGYQDGRPGDRRAEKGPAPKPTGQKMLDNLQKSENPRDPLFMAVLQNRHEMATYF 537
 DB 478 CRGYQDGRPGDRRAEKGPAPKPTGQKMLDNLQKSENPRDPLFMAVLQNRHEMATYF 537
 QY 481 CRGYQDGRPGDRRAEKGPAPKPTGQKMLDNLQKSENPRDPLFMAVLQNRHEMATYF 536
 DB 481 CRGYQDGRPGDRRAEKGPAPKPTGQKMLDNLQKSENPRDPLFMAVLQNRHEMATYF 536
 QY 538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSBARAFA 597
 DB 538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSBARAFA 597

DB 537 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSBARAFA 596
 QY 598 LTVARNCWSTTGLAHATEADAKAFPHQGVQVFLTRIMQGDMAAGPILRLGLAFLCF 657
 DB 597 LTVARNCWSTTGLAHATEADAKAFPHQGVQVFLTRIMQGDMAAGPILRLGLAFLCF 656
 QY 658 ALVTNLTTFSEEARPLRTGLEDLQDLSDLEKSPLYGQSRVVELVEAPAPQDGRGPA 717
 DB 657 ALVTNLTTFSEEARPLRTGLEDLQDLSDLEKSPLYGQSRVVELVEAPAPQDGRGPA 716
 QY 718 VELLTRMRKFGAVTVPLGNVVMYFAFLFTYVLLVDFRPPQSGSEVTLTFVWFT 777
 DB 717 VELLTRMRKFGAVTVPLGNVVMYFAFLFTYVLLVDFRPPQSGSEVTLTFVWFT 776
 QY 778 LVSEIQGFPTDDTHLVKKEFTLVBDNNKCMVAIPLFTVGTQRMPSAREAGTV 837
 DB 777 LVSEIQGFPTDDTHLVKKEFTLVBDNNKCMVAIPLFTVGTQRMPSAREAGTV 836
 QY 838 LAMDFVFTLRLLHIFAIHQLGPKIIVERMRKDVFFFLFPLSVMLVAYVTTQALLHP 897
 DB 837 LAMDFVFTLRLLHIFAIHQLGPKIIVERMRKDVFFFLFPLSVMLVAYVTTQALLHP 896
 QY 898 HDGRLWIFRRVLYRPLQIFGQIPLDEIDARVNCSTHPLLEDSPSCSLYANWIVL 957
 DB 897 HDGRLWIFRRVLYRPLQIFGQIPLDEIDARVNCSTHPLLEDSPSCSLYANWIVL 956
 QY 958 LLYVFLVTVNLVNLNLIIMSYTFQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1017
 DB 957 LLYVFLVTVNLVNLNLIIMSYTFQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1016
 QY 1018 SHLSLTLRVRVEKAEHREHLERDLPDPLQKVVMTQVQVQVQVQVQVQVQVQVQV 1077
 DB 1017 SHLSLTLRVRVEKAEHREHLERDLPDPLQKVVMTQVQVQVQVQVQVQVQVQVQV 1076
 QY 1078 LKTAHVRVDIAKYIGLREQEKRIKLESQINQSVLVSSVADVLAAQGG 1127
 DB 1077 LKTAHVRVDIAKYIGLREQEKRIKLESQINQSVLVSSVADVLAAQGG 1126
 QY 1078 LKTAHVRVDIAKYIGLREQEKRIKLESQINQSVLVSSVADVLAAQGG 1127
 DB 1077 LKTAHVRVDIAKYIGLREQEKRIKLESQINQSVLVSSVADVLAAQGG 1126
 RESULT 6
 Q9EPM3 PRELIMINARY; PRT; 1116 AA.
 ID Q9EPM3
 AC Q9EPM3
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Ltrpc5 protein.
 GN TRPM5 OR LTRPC5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RA MEDLINE=20377495; PubMed=10915772;
 RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
 RA Davies K., Reinhardt R., Reik W., Walter J.;
 RT "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RL Hum. Mol. Genet. 9:1829-1841(2000).
 DR EMBL; AJ251835; CAC19457.1; -.
 DR MGD; MGI:1861718; Trpm5.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_channel_TrpL.
 DR Pfam; PF00520; Ion_trans_1.
 KM Ionic channel; Transmembrane.
 SQ SEQUENCE 1116 AA; 126608 MW; 32DFABCF2835E48 CRC64;
 Query Match 81.5%; Score 4963.5; DB 11; Length 1116;
 Best Local Similarity 85.6%; Pred. No. 0;
 Matches 954; Conservative 60; Mismatches 93; Indels 7; Gaps 3;

```

QY 1 MODVCGRRPGSGDAEDRRELGLHREGEVNFSGSGKKRGKFEVAVPSGVAPSVLFDLLLEW 60
Db 1 MOTTSSCGSGPPTDEGMEPLCRGEINFGSGKKRGKFEVAVPSGVAPSVLFEELLLEW 60
QY 61 HLPAPNLVSLVGEBOFPAMKSMRLDVLRKGLVKAQOSTGAMILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSLVGEBOFPAMKSMRLDVLRKGLVKAQOSTGAMILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKVRVAVAGMAGSLGRVLRHRL- EAQEDFPVHYBEDDGGSGPLCSLDS 178
Db 121 RDHSLASTSTKVRVAVAGMAGSLGRVLRHRL- EAQEDFPVHYBEDDGGSGPLCSLDS 178
QY 179 NLSHFLVSGALGSGNDGLTEQSLERKHSIQRTGYGCTSCIQIPVCLLVNGDPNTL 240
Db 179 NLSHFLVSGALGSGNDGLTEQSLERKHSIQRTGYGCTSCIQIPVCLLVNGDPNTL 240
QY 238 ERISSRAVEQAAPMLILVSGGIADVLALVNOPHLVPRVAKOPKEKPSKHFMSMEDIV 297
Db 238 ERISSRAVEQAAPMLILVSGGIADVLALVNOPHLVPRVAKOPKEKPSKHFMSMEDIV 297
QY 241 ERISSRAVEQAAPMLILVSGGIADVLALVNOPHLVPRVAKOPKEKPSKHFMSMEDIV 300
Db 241 ERISSRAVEQAAPMLILVSGGIADVLALVNOPHLVPRVAKOPKEKPSKHFMSMEDIV 300
QY 298 RMTKLLONTSHOHLITVDFEBOGSEELDTVILKALVACSHSGSEPDYIDELKLAVA 357
Db 298 RMTKLLONTSHOHLITVDFEBOGSEELDTVILKALVACSHSGSEPDYIDELKLAVA 357
QY 301 HMTTELLQNTAAHPHLITVDFEBOGSEELDTVILKALVACSHSGSEADYIDELKLAVA 360
Db 301 HMTTELLQNTAAHPHLITVDFEBOGSEELDTVILKALVACSHSGSEADYIDELKLAVA 360
QY 358 MWRVIDAKSEIFNGDVEMKSCDLEEVMTDALVSNKPEFRLFPVNDGADVADFLTYGRLOE 417
Db 358 MWRVIDAKSEIFNGDVEMKSCDLEEVMTDALVSNKPEFRLFPVNDGADVADFLTYGRLOE 417
QY 361 MWRVIDAKSEIFNGDVEMKSCDLEEVMTDALVSNKPEFRLFPVNDGADVADFLTYGRLOE 420
Db 361 MWRVIDAKSEIFNGDVEMKSCDLEEVMTDALVSNKPEFRLFPVNDGADVADFLTYGRLOE 420
QY 418 LVRSVRSKSLFDLLQROKOEABRLTLAGLGTQOAREPPVAPAFSLHESRVLKPLQDA 477
Db 418 LVRSVRSKSLFDLLQROKOEABRLTLAGLGTQOAREPPVAPAFSLHESRVLKPLQDA 477
QY 421 LVHSVPSKSLFDLLQROKOEABRLTLAGLGTQOAREPPVAPAFSLHESRVLKPLQDA 480
Db 421 LVHSVPSKSLFDLLQROKOEABRLTLAGLGTQOAREPPVAPAFSLHESRVLKPLQDA 480
QY 478 CRGFYODGPGDRRRAEKGPAPKPTGQKWLILNQSENPRMDLFLMANVLQNRHEMATTF 537
Db 478 CRGFYODGPGDRRRAEKGPAPKPTGQKWLILNQSENPRMDLFLMANVLQNRHEMATTF 537
QY 481 CRGFYODGPGDRRRAEKGPAPKPTGQKWLILNQSENPRMDLFLMANVLQNRHEMATTF 536
Db 481 CRGFYODGPGDRRRAEKGPAPKPTGQKWLILNQSENPRMDLFLMANVLQNRHEMATTF 536
QY 538 NMGOGSGVAAALAAKILKEMSHLETAEABARA TREAKYERLALDIFSCYSSEBARA 597
Db 538 NMGOGSGVAAALAAKILKEMSHLETAEABARA TREAKYERLALDIFSCYSSEBARA 597
QY 537 NMGOGSGVAAALAAKILKEMSHLETAEABARA TREAKYERLALDIFSCYSSEBARA 596
Db 537 NMGOGSGVAAALAAKILKEMSHLETAEABARA TREAKYERLALDIFSCYSSEBARA 596
QY 598 LVRRNRCKWGA PVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 777
Db 598 LVRRNRCKWGA PVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 777
QY 597 LVRRNRCKWGA PVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 776
Db 597 LVRRNRCKWGA PVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 776
QY 658 ALVYTLITFSEBAPRTGLEDLQDLSLDTESPLVGLQSRVEELVAPRAQDGPRA 717
Db 658 ALVYTLITFSEBAPRTGLEDLQDLSLDTESPLVGLQSRVEELVAPRAQDGPRA 717
QY 657 ALVYTLITFSEBAPRTGLEDLQDLSLDTESPLVGLQSRVEELVAPRAQDGPRA 716
Db 657 ALVYTLITFSEBAPRTGLEDLQDLSLDTESPLVGLQSRVEELVAPRAQDGPRA 716
QY 718 VPLLTRMRKMGAPVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 777
Db 718 VPLLTRMRKMGAPVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 777
QY 717 APLLTRMRKMGAPVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 776
Db 717 APLLTRMRKMGAPVTVFIGNVVMYFAFLFTYVLLVDRPPPOGSPSGEVLTYFMVFT 776
QY 778 LVLEERIOGFFTEDETHLVKFFLTYVGDMMNKCDAVAILFLIVGTCRMLPSA FEAGRTV 837
Db 778 LVLEERIOGFFTEDETHLVKFFLTYVGDMMNKCDAVAILFLIVGTCRMLPSA FEAGRTV 837
QY 777 LVLEERIOGFFTEDETHLVKFFLTYVGDMMNKCDAVAILFLIVGTCRMLPSA FEAGRTV 836
Db 777 LVLEERIOGFFTEDETHLVKFFLTYVGDMMNKCDAVAILFLIVGTCRMLPSA FEAGRTV 836
QY 838 LANDFVFTLRLLIHAIRKQLCPKIIIVERRMKOVFFFLFETSWLVAVGTTQALLHP 897
Db 838 LANDFVFTLRLLIHAIRKQLCPKIIIVERRMKOVFFFLFETSWLVAVGTTQALLHP 897
QY 837 LAIDFVFTLRLLIHAIRKQLCPKIIIVERRMKOVFFFLFETSWLVAVGTTQALLHP 896
Db 837 LAIDFVFTLRLLIHAIRKQLCPKIIIVERRMKOVFFFLFETSWLVAVGTTQALLHP 896
QY 898 HDRLRMIIPRRVLYRPLQIFGOIPLDEIDEARVNGSTHPLLEDSPGSCSLAANMLVIL 957
Db 898 HDRLRMIIPRRVLYRPLQIFGOIPLDEIDEARVNGSTHPLLEDSPGSCSLAANMLVIL 957
QY 897 HDRLRMIIPRRVLYRPLQIFGOIPLDEIDEARVNGSTHPLLEDSPGSCSLAANMLVIL 956
Db 897 HDRLRMIIPRRVLYRPLQIFGOIPLDEIDEARVNGSTHPLLEDSPGSCSLAANMLVIL 956
QY 958 LVLTFPLVTNLMLNLIAFSYTFQVVOGNAATFMFKORYNLIVETHERPALAPFILL 1017
Db 958 LVLTFPLVTNLMLNLIAFSYTFQVVOGNAATFMFKORYNLIVETHERPALAPFILL 1017
QY 957 LVLTFPLVTNLMLNLIAFSYTFQVVOGNAATFMFKORYNLIVETHERPALAPFILL 1016
Db 957 LVLTFPLVTNLMLNLIAFSYTFQVVOGNAATFMFKORYNLIVETHERPALAPFILL 1016
QY 1018 SHLSLTLRVFKKAEHKEHLEBDLPDLQKVVTWETVQKENFLSKMEKRRDSEGEV 1077
Db 1018 SHLSLTLRVFKKAEHKEHLEBDLPDLQKVVTWETVQKENFLSKMEKRRDSEGEV 1077
QY 1017 SHLSLTLRVFKKAEHKEHLEBDLPDLQKVVTWETVQKENFLSKMEKRRDSEGEV 1076
Db 1017 SHLSLTLRVFKKAEHKEHLEBDLPDLQKVVTWETVQKENFLSKMEKRRDSEGEV 1076

```

```

QY 1078 LRKTAHRVDLAKYVGLGLEQEKRIKCLSEGINY 1111
Db 1077 LRKTAHRVDLAKYVGLGLEQEKRIKCLSEGINY 1110
RESULT 7
Q8BS44 PRELIMINARY; PRT; 1030 AA.
AC Q8BS44
ID Q8BS44
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Transient receptor potential cation channel (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK035197; BAC28976.1;
FT NON-TER 1
SQ SEQUENCE 1030 AA; 116983 MW; DDB31B7DF238F402 CRC64;

Query Match 73.0%; Score 4445.5; DB 11; Length 1030;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 856; Conservative 55; Mismatches 94; Indels 11; Gaps 3;

QY 151 LEEAEDPPVHYREDDGGSGPLCSLDSNLSHFLVYEGPPEKG-DGLTELRRLREKHS 209
Db 25 LSLAEDPPPIHYPADEGNIOGPLCPDNLSHFLVYEGALGSGNDGLTEQLSLEKHS 84
QY 210 EORAGYGGTSGIEIPVLCILVNGDPTLERISRAVEQAAPMLILVSGGIADVLALVNO 269
Db 85 QORTGYGCTSCIQIPVLCILVNGDPTLERISRAVEQAAPMLILVSGGIADVLALVNO 144
QY 270 PHLLVPRVAKOPKEKPSKHFMSMEDIVRMTKLLONTSHOHLITVDFEBOGSEELDTV 329
Db 145 PHLLVPRVAKOPKEKPSKHFMSMEDIVRMTKLLONTSHOHLITVDFEBOGSEELDTV 204
QY 330 ILKALVYKCKSHSGPODYLDELKLA VMDRVDAKSEIFNGDVEMKSCDLEEVMTDALV 389
Db 205 ILKALVYKCKSHSGPODYLDELKLA VMDRVDAKSEIFNGDVEMKSCDLEEVMTDALV 264
QY 390 SNKPEFVRLEFVNGADVADFLTYGRLOELYRSVRSKSLFDLLQROKOEABRLTLAGLGTQ 449
Db 265 SNKPEFVRLEFVNGADVADFLTYGRLOELYRSVRSKSLFDLLQROKOEABRLTLAGLGTQ 324
QY 450 QAREPPAGPAFSLHESRVLKDFLODACRGFYODGRRRAEKGPAPKPTGQKWLID 509
Db 325 QAREPPAGPAFSLHESRVLKDFLODACRGFYODGRRRAEKGPAPKPTGQKWLID 380
QY 510 LMOKSENPRMDLFLMANVLQNRHEMATTFYFAMQOEGVAAALAAKILKEMSHLETAEABAR 569
Db 381 LSRKSEDPWRDLFLMANVLQNRHEMATTFYFAMQOEGVAAALAAKILKEMSHLETAEABAR 440
QY 570 ATREAKYERLALDIFSCYSSEBARAFALVRRNRCKWGA PVTVFIGNVVMYFAFLFTY 629
Db 441 TMEBAKTEBQALDLPSECGNSSEBARAFALVRRNRCKWGA PVTVFIGNVVMYFAFLFTY 500
QY 630 QAFLTRIWMGMAAGTPILRLGAFALVYTNLITFSEBAPRTGLEDLQDLSLDT 689
Db 501 QAFLTRIWMGMAAGTPILRLGAFALVYTNLITFSEBAPRTGLEDLQDLSLDT 560
QY 690 KSPLYGQSRVEELVAPRAQDGPRAVFLTRMRKMGAPVTVFIGNVVMYFAFLFTY 749
Db 561 KSPLYGQSRVEELVAPRAQDGPRAVFLTRMRKMGAPVTVFIGNVVMYFAFLFTY 620

```

```

QY 750 TVLLVDFPPPPGSGSEVTVLVFVTVLVEIRGSEFTEDTHLVKKFTLVYGDNNK 809
DB 621 TVLLVDFPPPPGSGSEVTVLVFVTVLVEIRGSEFTEDTHLVKKFTLVYEDNNK 680
QY 810 CDMVALFELTVGVTCGMLPSAFBAGTVALMPVMTLLLIHFAHKOLGKIIYVEM 869
DB 681 CDMVALFELTVGVTCGMLPSAFBAGTVALMPVMTLLLIHFAHKOLGKIIYVEM 740
QY 870 MDVFFELFELSVMLVAVYVTTQALLPHDGRLEWIFRRVLYRPYQIFGQIPLDEIDA 929
DB 741 MDVFFELFELSVMLVAVYVTTQALLPHDGRLEWIFRRVLYRPYQIFGQIPLDEIDA 800
QY 930 RVNCSHPLLEDSPSCPSLYANMVLILLVTVLTVNVLNMLLIAMFSYTFQVQVNA 989
DB 801 RVNCSHPLLEDSPSCPSLYANMVLILLVTVLTVNVLNMLLIAMFSYTFQVQVNA 860
QY 990 TMFMFORNYLVEYHERPALAPFLLSHLSLTRVFKKAENKREHLEDDLPPLDQ 1049
DB 861 DMFMFORNYLVEYHERPALAPFLLSHLSLTRVFKKAENKREHLEDDLPPLDQ 920
QY 1050 KVVTEVQKENFLSKMEGRDSEGEVLRKTAHRYDFAKYLGRLREGEKIKCLESGQ 1109
DB 921 KVVTEVQKENFLSKMEGRDSEGEVLRKTAHRYDFAKYLGRLREGEKIKCLESGQ 980
QY 1110 NYCSSLVSVADVLAQGGGPRSSOHGEGSOLVAADHRGIDGWEPGAGPPSDT 1165
DB 981 NYCSSLVSVADVLAQGGGPRSSOHGEGSOLVAADHRGIDGWEPGAGPPSDT 1030

```

RESULT 8

```

Q8TD43 08TD43 PRELIMINARY; PRT; 1214 AA.
AC Q8TD43;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Cation channel TRPM4B.
GN TRPM4B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Perraud A.-L., Scharenberg A.;
RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF497623; AAM18083.1; -.
DR Genew; HGNC:17993; TRPM4.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; ion_trans_1.
KW Ioni channel; Transmembrane.
SQ SEQUENCE 1214 AA; 134300 MW; 76AD4452690EDBFS CRC64;

```

Query Match 39.9%; Score 2430.5; DB 4; Length 1214;
 Best Local Similarity 45.4%; Pred. No. 2,3e-179;
 Matches 532; Conservative 177; Mismatches 352; Indels 111; Gaps 26;

```

QY 26 GEVNFSGGSKRGKRVVPSVAVSVLPULLLAEMHLPAPNLVSLVGEOPFANKSWLR 85
DB 76 GELDTGAGRKSNFLRLSDRTDPAVYSLVTRWGFRAPNLVSVVLGSGGSPVLTQMLQ 135
QY 86 DVLARGVLAASOSTAMILTSALRVGLAHNGQAVRDHSLASTSTKRVVANGMSLGRV 145
DB 136 DVLARGVLAASOSTAMILTSALRVGLAHNGQAVRDHSLASTSTKRVVANGMSLGRV 194
QY 146 LHRRLLEAQBDFPVHY-----PEDDGSQGLCSLDSNLSHFIVEPGRPKGDLTEL 200
DB 195 RNRDRLINKSGSPARVWRGDPED--GVQFP---LDYVSAFLVDDGTHGCLGGENRF 249
QY 201 RLRLKHSIQAGVGGTGSIEIPVLCILVNDPMTLERISRAVDAQAWMLIVSGGIA 260

```

```

DB 250 RLRLHSYSQKTVGGTb-IDIPVLLLLIDGDEKMLTRINENATQAOLPCLLVAGSGGA 308
QY 261 DVLAALVNPMLVb-----KVAEQKFEKFPKSHFSWEDIVMTKLLQNTSHOHL 313
DB 309 DCLATLTED--TLAAGSGAROGEARDRIRRFPR-----GDLEVLQAOVENIMRKELL 361
QY 314 TVYDFEQGSEELDTVILKALVKACKSHSQEBODYLDELKLAIVAMDRIYAKSEIFNGDV 373
DB 362 TVYSSb-DGSEEFITVILKALVKAC--CSSEASAVLDELRLAVANNRVDIAQSEIFRQDI 418
QY 374 EWSGCDLEWMDALVSNKPEFVRLFVNGADVADPFLTYGRLQELIYRSRSKSLPDLLO 433
DB 419 QMRSHLASLMDALNDORPEFVRLISHGLFHTPMRLAQDYSAFNSLRNLRLND 478
QY 434 RKEBARLTLAGL--GTQOAREPPAGPAPFSLHEYSRVLDPLQACRGFYDODGRPDR 491
DB 479 QASHAGTRKAPALKGAALRRP-----DVGHVRLMLGKACAPRYISGGAWDH 528
QY 492 RAKEGPAPRPTGQKVLIDLNOKS-----ENPARDLFLVAVLQNRHEMATYFWAMQ 542
DB 529 -----PGQOFBSVYLLSDKATSPSLDAGLQAPWSDULLMALLLNRAQWAMYFMEKGS 583
QY 543 EGVAAALAACTLKEMSHLETAEAARATREA--KYERLADLSECTSNSERAPALLV 600
DB 584 NAVSSALACCLLRVWARLEPDAEBAARKDLAFKEGVDLFFEGCYRSSSEVRAARLL 643
QY 601 RNRCSMTTCLHLTEADAKAFPAHDGVQAFTRIMGDMAGPTIRLILGAFCPALV 660
DB 644 RRCPLMGATCLQLMADARAFPAODGVOSLITKMGDMASTPPIVALVLAFFCPLI 703
QY 661 YTNLITF--SEBAPRLTGLEDLQDLSLDTESKPLYGQSRVEELVEAPRAGD----- 712
DB 704 YTRLITFKRSEEPFRELE--FQMDSYINGGPVGTADPAKFTLGVPRGGRGCCGG 761
QY 713 --RGRPAVFLTRWKEFGAPTYVFLGVNVMFAPLFTYVLLVDFPPPPGSGSEVTV 770
DB 762 RCGGRRC--LRMWHFGAPVITFMGNVSYLLFLLLFSLVLDVDFOPAP--PGLLEL 816
QY 771 LYFWFTVLEIRGSEFTEDT-----HLVKKFTLVYGDNNKCDMVAIPLFI 819
DB 817 LYFWFTVLEIRGSEFTEDT-----HLVKKFTLVYGDNNKCDMVAIPLFI 876
QY 820 VGVTCRMLPSAFBAGTVALMPVMTLLLIHFAHKOLGKIIYVERMKDVFPLFF 879
DB 877 LGVGRRLRPLGLYHGRVLCIDFMVFTVRLHIFVNNQOLGKIIYVERMKDVFPLFF 936
QY 880 LSWLVAVYVTTQALLPHDGRLEWIFRRVLYRPYQIFGQIPLDEIDARV--NCSTH 936
DB 937 LGVWLVAAGVATEGILRPRSDPFSILRRVFYRPYQIFGQIPQEDMDVALMEHSCSE 996
QY 992 FLMFQRYNLIVEYHERPALAPFLLSHLSLTRVFKK-----EAEKREHLEDD 1042
DB 997 PEFMAHPGAQAGTCSOTYANMLVLLVTFILVANNILLVNLIIAMFSYTEKVGNSDL 1056
QY 1043 LPDPLDQVTVQKENFLSKMEGRDSEGEVLRKTAHRYDFAKYLGRLREGEKRI 1102
DB 1117 -----AERKLITWESVHKNFLARARDKRESDESRLKTSQVDLALKOLGHIRVEQRL 1172
QY 1103 KLESQIYNYCVSVSVADVLAQ-----GCP 1129
DB 1173 KVLREVOQCSRVLGVAEALSRSALLPPGGP 1204

```

RESULT 9

```

Q96L84 096L84 PRELIMINARY; PRT; 1040 AA.
AC Q96L84;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

```



```

QY 413 GRLOELYSVSRKSLFLDLOKQOEANLTLAQL--GTQOAREPPAGPPASLHEVSRL 470
D 284 MRLAQVLSAAPSNSLIRNLDQASHAGTAKAPALKGAAELRPP-----DVGHVL 333
QY 471 KDFLODACRGFQODRPGDRRAEKGPAKRTGQKMLDLNQS-----ENPWRDL 521
D 334 RMLGKMCAPRYPSGGAMPD-----PQGGEGSNVLLSDKATSPSLDAGLGQAPWSDL 388
QY 522 FLMAVLQNRHEMATYFMAWGOEVAALAAACKILKEMSHLETEAARATREA--KYERL 579
D 389 LLMALLNRAQAMAYFMEMGSNAVSSALGACILLVMARLEPDAEAAARKDLAKFKGM 448
QY 580 ALDIFSECSNSSEARAFALLVRRNCWSKTTGLHATADAKAFPAHDQVQAFLTRIMWG 639
D 449 GVDIFGECYRSSEVAARLLLRCPMGDATCLQAMQADARAFPAQGVOSLTLQKWMG 508
QY 640 DMAACTPLRLILGALCFALVYTNLITF--SEAPLRGLLELODLSLDEKSPYLGLQ 697
D 509 DMASTPLMALVLAFFCPLLYTRLITRKSEEPTRKELE--FMDSDVINCEGVTAD 566
QY 698 SRVEELVAPRAQD-----RGPRAVFLTRRKFMGAPVTVFLGNVWYFAFLFLF 749
D 567 PAETPLGVPVROSGRPGCCGRCGRRC--LRKFHMGAPVTLFMGNVSYLLFLFLF 623
QY 750 TYVLLVDRPPQSGSEVTLVFWVFTLVLEIRQGFTEDETL-----HLVKK 798
D 624 SRVLLVDFOPAP--PGLELLLYFWAFLLCEBLAQSLSGGGSLASGPGPHASLSQR 681
QY 799 FTLVGDWVNCMDVAIFLTVGTCRMLPSAFEGRTVLAAMDVWVFTLRLIHFAHKQ 858
D 682 LRLVLABSWNOCDLVALTCFLGVCGRLLPLGLYHIGRTVLCIDFVWFTVRLHITVKQ 741
QY 859 LGPKIIVERRMKDVFFFLFSLVWLVAVGVTQALLPHDGRLEWIFRRVLYRPLQIF 918
D 742 LGPKIVISKMKDVFFFLFGLVWLVAVGATBELLPDSDPSILRRFYRPLQIF 801
QY 919 GOIPLDEIDEARV--NCSTHPLLEDSR-----SCPSLYANWLVILLVFTLVNTVL 970
D 802 GOIPOEDMDVALMEHNSCSEBGFWAHPGAQGTCSQYANWLVILLVFTLVNTVL 861
QY 971 MLLIAMSTYFOVYQNAATFMKQRYNLIVETHERALAPPLLSLTLRLRVFKK 1030
D 862 VLLIAMSTYFGKQNSDLYWKAQRYRLIRFHSRPLALPPFVISHLLRLQLCR 921
QY 1031 -----BAEHKREHLERDLPDLQKVTVTWVQENFLSKMEKRKRSSEGVLEKT 1081
D 922 PRSPOSSPALHEHRYLSKE--AERKLLTWESVHKENFLADARDKRESDESRLERT 977
QY 1082 AHRVDFIAKYLGLREDEKRIKLESQINYS 1113
D 978 SQKVDLALKOIGHIREYQRLKVLEREVOQS 1009

```

RESULT 11
Q8BLM7 PRELIMINARY: PRT: 945 AA.

AC Q8BLM7;
DT 01-MAR-2003 (Tremblrel. 23. Created)
DT 01-MAR-2003 (Tremblrel. 23. Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23. Last annotation update)
DE Similar to TRP-related cation influx channel.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N. A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=2354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

```

RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK044094; BAC31771.1;
SQ SEQUENCE 945 AA; 105526 MW; B7261C0A368866EB CRC64;

Query Match 33.7%; Score 2051; DB 11; Length 945;
Best Local Similarity 45.6%; Pred. No. 4.8e-150;
Matches 453; Conservative 141; Mismatches 276; Indels 124; Gaps 27;

QY 100 GAWILTSALRGALRHVQOARHDSIASTSKVAVNAGMSLGRVLRHRTLEAQDPP 159
D 4 GAWILVTGSLHTGIGHGVAVRDHQTASTGSS--KVAVAGVAPWGVNRRDMLINKGSPF 62
QY 160 VHY-----PEDDGSQGPLCISLDSNLSHFILVERPCPPGKGLTELRLEKHSIORAG 214
D 63 ARYMRGPED--GVEFF--LDVNSAFFLVDGCTYRGLGENRFLRFESVYVQOKTG 117
QY 215 YGTSISIEIPVLCILVNGDPNTLERISRVAQOAPWMLVSGSGIADVLAALVNOPHLV 274
D 118 VGGTG-IDIPVLLLLIDGDEKMLKRIEDATAQALPCLLVAGSGGAADCVETLED--TLA 174
QY 275 P-----KVAEKQPKKEFPKSHSWEDIVWTKLONITSHOHLTYVDQESSELD 327
D 175 PGSGGLRGEARDIRRYFPK-----GDPEVLAQOVERIMTRKELTYSSB--DSBEFE 228
QY 328 TVILKALVKAACKSHSQEPDYLDELKLAAMDVPIAKSEIFNGDVEMKSCDLEEWVDA 387
D 229 TIVRALVAKC--GSSESAVLDELRLAVANMRNDIAOSELPFRDIOHRSFHEASLMDA 286
QY 388 LVSNKPEFVRLVNDGADVADFLTYGRLOELYSVSRKSLFLDLOKQOEANLTLAQLG 447
D 287 LLNRPPEFVRLISHGLSHGFLTPVRLAQLYSAVSPNSLIRNLDQASH----- 336
QY 448 TQOAREPPAG-----PPASLHVSRLKDFLODACRGF-----ODGRPDR 490
D 337 ASSSKSPVNGTVELRPP-----NVGOVLRLLAETCAFPARPARTRDSYLGQHREND 390
QY 491 RRAEKGPAPRTGQKMLDLNQS-----SENPWRDLFLMAVLQNRHEMATYFMAWGO 542
D 391 -----SLMDANKOPSTDASEQAPWMDLILMALLNRAQNAIYFWEKGS 436
QY 543 EGVAAALAAACKILKEMSHLETEAARATRE--AKYERLALDIFSECSNSSEARAFALLV 600
D 437 NSVASALGACILLVMARLESEAEAAARKDLAATFMSMSVDLGECHNSEEBAARLL 496
QY 601 RRRNCWSKTTGLHATADAKAFPAHDQVQAFLTRIMGMAAGTPIRLILGALCFALV 660
D 497 RRCPLMEBATCLQAMQADARAFPAQGVOSLTLQKWMGEMDSTPIWALLLAFCCPLI 556
QY 661 YTNLITF--SEAPLRGLLELODLSLDEKSPYLGLQSVLEELVAPRAQGRGPRAV 718
D 557 YTNLIVRKSEEBEFTQOLD--FMDSSINGAGPGTVEBSAKVLE--RRORRRPGAL 612
QY 719 F--LITRRKFMGAPVTVFLGNVWYFAFLFTLVLLVDFRPPQSGSEVTLVFWV 775
D 613 CCGKFSKMSDFKAPVTAFLGNVSYLLFLFLFAHLVLDFOPTK--PSSELLTYMA 670
QY 776 FTLVLEIRQGF-----FTDEDTHLVKKFTLYVGDWVNCMDVAIFLTVGTC 824
D 671 FTLLCEBLRQGLGGWMSLASGGRPDRAPIRRLHLYLSDPTWVQCCLALTCFLGVC 730
QY 825 RMLPSAFEGRTVLAAMDVWVFTLRLIHFAHKQLGKTIYVENMMKDVFFFLFSLW 884
D 731 RLTFGLFDLGRVTLCDPFMTFTLRLHIFVNNKQLGKPIVVSMMKDVFFFLFCWL 790
QY 885 VAVGVTTQALLPHDGRLEWIFRRVLYRPLQIFGQIPLDEIDEARV--NCS-----T 935
D 791 VAVGVATEGLRPPDRSLPSILRRVFRPLQIFGQIPOSEMDVALMIPGCSHRSWA 850
QY 936 HPLLEDSR--SCPSTYANWLVILLVFTLVNTVLNMLLIAMSTYFOVYQNAATMF 992
D 851 HP-----GPAVAGCVCVSYANWLVILLVFTLVNTVLNMLLIAMSTYFYSKVHGNSDLY 906

```


QY 993 WKFORNLIVEHBPALAPPELLSHSLTLRR 1026
 DB 907 WKQORYSLREFHSPALAPPELLICHVSVRK 940

RESULT 12
 091YD4 PRELIMINARY; PRT: 1507 AA.

ID 091YD4
 AC 091YD4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Transient receptor potential channel 7 (fragment).
 GN TRP7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Kashiwa V.1
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ344343; CAC69081.1; -
 DR InterPro: IPR002311; Cat_channel_TrypL.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR002052; N6_Mtase.
 DR InterPro: IPR000086; NUDIX_hydrolase.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF00293; NUDIX; 1.
 DR PROSITE: PS00092; N6_MTASE; 1.
 DR Ionc channel; Receptor; Transmembrane.
 KM NON_TER 1507 1507
 SQ SEQUENCE 1507 AA; 172364 MW; 86552DE25939785 CRC64;

Query Match 33.2%; Score 2024; DB 11; Length 1507;
 Best Local Similarity 39.1%; Pred. No. 1,3e-147;
 Matches 449; Conservative 133; Mismatches 386; Indels 120; Gaps 22;

QY 26 GEVNFSGSKGKGFVBPVSPVAFVLLLAEMHLPAPNLVSLVGEOPFAMKSWR 85
 DB 127 GVIVFDLSQKVGKVRVSDPTSSVYQDLMQHMGLDVPNLLISVTGAKNFMMLRLK 186

QY 86 DVLRKGLVQAAGSTGMIILTSALRVGLAHVGOAVNDHSLASTKRVVAVAGMAGLGV 145
 DB 187 SJFRRGLVVAQTGTGMIITGSGHTGMQVGAVDFFSLSSCKGGEVITTGVAWTGTT 246

QY 146 LHRRIIEBAQEDPVHYPPEDDGGSGPLCSLDNLSHFILVEGPGKDGTLRLRL 205
 DB 247 HNRBGLIHPWGGFPAEYMLDEEG-OGNLTCGLDSNHSHPILVDGTGQGVETPLTKLE 305

QY 206 KHISEORAGYGTGSIPIVLCILVNGDPNTERISRAVEQAAPWILVSGGDIADVLA 265
 DB 306 KFISEQTKRGGV-AIKIPICVVLGGPCTHTITVAINNGPPCIVIEGSGVADVIAQ 364

QY 266 LVNQP--HLIVPVAKQ--FEKFPKHFSEWDIVRTKLLONTSHOHLITVDFEQ 320
 DB 365 VATLPVSEITISLIQKLSIFQEMFET--FTENOIVEMTKKIQDIVRRQLTIFREGK 422

QY 321 EGSEEDTVTLKALVACKSHSQEPDQYLD-ELKLVAMRVNIAKSEIFNGDVEMWSCD 379
 DB 423 DGGQDDVVALQALLKASRQDHFGEHNMHOLKLAAMKRVIAKSEITTDQMKPAD 482

QY 380 LBEVNVDAVSNKPEFRLVFDGADVADFLYGRLOELVRSVRKSLFDLLQR-KQEE 438
 DB 483 LHPMMTAAIISNPEFRFLFLENGVRKEVETWDTLLCTVENLEPSCLFPSKLOKVLAEE 542

QY 439 ARITLGLGTQARPPAGPPARSLEHVSRYLKDFLQDACKRGYQDGRPDERRAE---- 494
 DB 543 QRLAAYA-----SATPRLHMHVAVQLRELLDSTQLLYPRRYDRRLSMTPV 591

QY 495 -----KGPAPKPTGQ-KMLLDLNQKSENPMEDLFLMVLQVRHEMATYFPMAGQ 542

DB 592 HIKLVNGVSLRSYKSTGHTVFETID-----PVRLLIWAVYQNRRELAGIIMASQ 644
 QY 543 EGVAALAAACILLEMSHLE--TEABARATREAKYERLADLPSECSNSEARAFALV 600
 DB 645 DCTAALAKSKILKELSEEDTDSSEMLALADEFERAIGVTECRKBEEROKLV 704

QY 601 RNRNCSKTTGCIHLATEADAKAPFAHDVQAFTRIMWGMMACTPIRLLAGFLCFALV 660
 DB 705 RVSEAMGTTTQGLALEKDKMFPVSHGIGQAFITVVMWGCVDNGLWRILICMLAFPL 764

QY 661 YTNLITSEEARPLRTGLEDLDLDDLSLDTKSPYLGQSRVEVLEAPRQAQDGRRAFL 720
 DB 765 FTGFISFREK-----RLQALCRPAV----- 785

QY 721 LTRMKKFGAVTVTELGWVWVPAFLFTYVLLVDPFRPPGSPGSPETLYFVFTVTL 780
 DB 766 ---RAFNAPVAFVPMNLLSYFAFLCLFAVLMVDFP---SPSCYLLIYMLFSLVC 838

QY 761 EIRQGFPTDED-THLVKKFTLVYGDNNMKDMVAIFLPIVGTCTMLPSAFEAGRTVLA 839
 DB 839 BETROYLYTDPDGGGLMGMASISYFSDPNNKLDVGAILLFIYGLTCRLIPATLYPGRIILS 898

QY 840 MDFWVFTLRLIHIFAIHKQLGPKTIIVERMKDVFPLFPLSVLVAVGTTOALLPHPD 899
 DB 899 LDFIMFCLRLMHIETISKTLGPKTIIVKRMKDVFFFLFLAVWVSGVAKQAILIHNE 958

QY 900 GLEWIFFRVLYRPLQIFGOIP--LDIDEARVNC--THPLLEDSPSGCS----- 948
 DB 959 SRVDWIFRGVAVHSLTTFGQIPYIDGVNFSMDCCSPNGTDPY---KPKCPESDWGQ 1014

QY 949 --LVANMIVILLVFLVTVNVLNMLLIAMFSYTFQVQVGNATFMKFORNLIYEHY 1006
 DB 1015 AFAPEWMLTVLLLCIYLPANILLNLIAMNVTFOEQEHTDQIMKQORHDLIEYHG 1074

QY 1007 RPALAPPELLSHSLTLRLVRFKKEAHEKREHLEDLPDLDQKYVTEVQENFPLSM 1066
 DB 1075 RPPAPPPELLSHSLTLRLIKRIVLKIPAKHKQIKKLEKNEETALLSMELYLEKYNLQ 1134

QY 1067 EKRRRDSGEVLRKTAHVRDFAKYL-----GGLEOEKIKLCESQINCSVLVSSV 1119
 DB 1135 QYQQAQRPQKQIDISEKVDIVDLDMDQVKSSTEO--RLASLEQVTOVTRALHMT 1192

QY 1120 ADVLAQGG 1127
 DB 1193 VTTLKDSG 1200

RESULT 13
 08R4D5 PRELIMINARY; PRT: 1104 AA.

ID 08R4D5
 AC 08R4D5;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE TRP ion channel TRPM8 (Transient receptor potential Ca++ channel TRPM8)
 GN TRPM8 OR TRPM8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA MEDLINE=21890731; PubMed=11893340;
 RA Peier A.M., Moglich A., Hergarden A.C., Reeve A.J., Andersson D.A.,
 RA Story G.M., Barley T.J., Dragon I., McIntyre P., Bevan S.,
 RA Patapoutian A.; that genes cold stimuli and menthol."
 RL Cell 108:705-715(2002).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Testis;

RA Tsavalier L., Laus R.:
 RT "The murine homologue of TRPM8 (Trpp8) gene: cloning, sequencing and
 RL tissue distribution."
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF481480; AAL79553.1; -
 DR EMBL: AY095352; AAM23261.1; -
 DR MGI: 2181435; Trpm8.
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR005821; Ion_trans.
 DR Pfam: PF00520; Ion_trans.1.
 KW Ionic channel; Receptor; Transmembrane.
 SQ SEQUENCE 1104 AA; 127709 MW; 1685D6FBD2BE96D CRC64;

Query Match 25.9%; Score 1578; DB 11; Length 1104;
 Best Local Similarity 33.4%; Pred. No. 3.4e-113;
 Matches 374; Conservative 207; Mismatches 392; Indels 148; Gaps 24;

QY 26 GEVNGSGGKRGKRVVPVSGVAPSVLPDLLAEMLPAPNLVSLVGEOPFANKSWLR 85
 DB 104 GDIOFETLGKK-GKYLRLSCDTSBETLYELLTQHMLKTPNLVIVITGGAKNFALKPRMR 162
 QY 86 DVLRKGLVKAAGSTGAMILTSALRGVLAHVGQAVRDHSLASTSTKRVVAAGMASLGRV 145
 DB 163 KIFSR-LVIYAKSGAMILTGTHYGLMKYIGEVARDNTI-SRSEENIYALGIAAMGV 220
 QY 146 LHRRLIEAOD---FVHYRPEDDGGSGPLCSLDSNLSHFILVEPGPGKDGLTETRL 202
 DB 221 SNRDLIRSCDBEGHFSAGYIMD-FTRDPLVILDNHNTLLVNDGCHGHTPEAKLRN 279
 QY 203 RLEKHISE---QRAYGCGTSGIEIPVLCVLVNGDPNTLERISRAVEQAAPMLIVGSGGI 259
 DB 280 QLEKISERTSDSNYGG---KIPVCFAGCGRETLKALINTSVKSKIPCVVVEGSGOI 335
 QY 260 ADVLAALVNOPHLVPAKAEKQFKEKFPSS-KHFSMEDIVMTKLLONTSHQHLTYVD 317
 DB 336 ADVIASLVEVEDVLTSSNWKELVFLPRTVSRLEPEEIESITKMKELLESCHLLTYIK 395
 QY 318 FEQSGSEELDTVILKALVAKCKSHQSEPODYDELKELAVAMDVIAKSEIFNGDVEWKS 377
 DB 336 MEEADDELVSNAISVALYKAFSTNQDKNNWQGLKLENNQDLADSEIFNDNRWES 455
 QY 378 CDLEVNVDALVSNKPEFVRLFDNGADVADFLTYGRLOELVRSYRSKSLFDELQ---R 434
 DB 456 ADLOVMFTALIKDRPKFVRLFLENGNLQKFLTNEVLELF-SYHSTFLVYRNLIQIAN 514
 QY 435 KOEERLTLAGCTQOARPRAPRASFSLHESRVLKQPLQACGFODGPRGRRAE 494
 DB 515 SYNDLALTF-----VWKLVANFR---RSFWEKEDR----- 540
 QY 495 KGPARKPTGOKWLLDNOKSENPRDLFLMAVLQNRHEMATYFMAQGOEVAALAAKCI 554
 DB 541 ---SRREDLVDELHSLTTRHRLQALFIMALQKKELSKIYOTGCTIALAAGAKL 597
 QY 555 LKESHSLETEADAPATREA-KYERLALDIFSECSYNSSEAPAFALLVRRNCWSTTCL 612
 DB 598 LKTLAKKNDINDIAAGESEELANEYETRAVELTECSYNDDELAQQLVYSCAAGSNCIL 657
 QY 613 HLATEADAKAPFAHGVQAFELTRIMWGDMAAGTPIRLGLAFLCALVYTNLITSEAP 672
 DB 658 ELAVEATDOHFIAQGVONFISKOMYGEISRTKMKIILCLFIPLVCGGIVSRKK-- 715
 QY 673 LRTGLEDDLDLDTESKSPYGLQSRVLEAPRAQODRPAVFLITRMKRWGAPV 732
 DB 716 -----PIDKHKK-----LLMYVAEFTSPF 735
 QY 733 TVFLCANVMPAFELFTYVLLVDRPPQSGSEVLTLYFWVFTLVLEIRQGFETD 792
 DB 736 VVFSNNVVFYIAFLLLFAVLLMDHVSVDH---TPELIYALVFLFCDEVQWYMGV 792
 QY 793 THLVAKFTLVYGDNNKCDMAVLEFIYGVTCRM---LPSAEARITVLANDFWFTLRL 849
 DB 793 -----YFTDLNVMMDTGLGFYIAGIVFRLHSSNKSLSYSGRVICLDYIIIFTLRL 843

QY 850 IHIFAIHQLOPKIIVVERMKVDYFFFLFSLVWLVAVGTTQALLPHDGLXENIFRRV 909
 DB 844 IHIFVSHNLGPKIMQRMIDVFFFLFAVMAVGARQGLRQNEGMRWIFRSV 903
 QY 910 LYRPLQIFGQIPDEIDAEVNC-----THPLLE-DSPCSPSLANMVLITLLV 960
 DB 904 IYEPYLAIFGVPSD-VDSITYVDHSCFTSGNESKPLCEVDEHNLPR-FPEWITIPVLC 961
 QY 961 TFLVTVNLVNLMLIAMFSYTFQVVGNAITFMFKFORNLIVYERPALAPPIYLSHL 1020
 DB 962 IYMLSTNLVNLVNLVAMGYVIGVQENNDQVYKFORFLVQVQCNRLNIPPFVPAVF 1021
 QY 1021 SLTLARVKEAEHREHLEBDLPDQKVYVETVQENFLSPMEKRRDSEGEVLAK 1080
 DB 1022 YVWVKKCFKCCCKEKMSNACCFRNEDENTLAEVGVKENYLVKINTKANDNS----- 1075
 QY 1081 TNRVDFIAYLGLGREQEKIKLESQINTCSLVSSVAD 1121
 DB 1076 -----EEMRHRFROLDSTLNDLSKILKEIAN 1101

RESULT 14

QY 08R455 PRELIMINARY; PRT; 1104 AA.

AC 08R455;
 DT 01-JUN-2002 (Tremblrel; 21, Created)
 DT 01-JUN-2002 (Tremblrel; 21, Last sequence update)
 DT 01-OCT-2002 (Tremblrel; 22, Last annotation update)
 DE Cold/menthol receptor 1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Trigeminal ganglion;
 RX MEDLINE=21877404; PubMed=11882888;
 RA McKemy D.D., Neuhauser W.M., Julius D.;
 RT "Identification of a cold receptor reveals a general role for TRP
 channels in thermosensation."
 RL Nature 416:52-58(2002).
 DR EMBL: AY072788; AAL68394.1; -
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR005821; Ion_trans.
 DR Pfam: PF00520; Ion_trans.1.
 KW Ionic channel; Receptor; Transmembrane.
 SQ SEQUENCE 1104 AA; 127651 MW; 0FBDED11FC025D09 CRC64;

Query Match 25.7%; Score 1563.5; DB 11; Length 1104;
 Best Local Similarity 34.0%; Pred. No. 4.6e-112;
 Matches 375; Conservative 205; Mismatches 395; Indels 129; Gaps 25;

QY 26 GEVNGSGGKRGKRVVPVSGVAPSVLPDLLAEMLPAPNLVSLVGEOPFANKSWLR 85
 DB 104 GDIOFETLGKK-GKYLRLSCDTSBETLYELLTQHMLKTPNLVIVITGGAKNFALKPRMR 162
 QY 86 DVLRKGLVKAAGSTGAMILTSALRGVLAHVGQAVRDHSLASTSTKRVVAAGMASLGRV 145
 DB 163 KIFSR-LVIYAKSGAMILTGTHYGLMKYIGEVARDNTI-SRSEENIYALGIAAMGV 220
 QY 146 LHRRLIEAOD---FVHYRPEDDGGSGPLCSLDSNLSHFILVEPGPGKDGLTETRL 202
 DB 221 SNRDLIRSCDBEGHFSAGYIMD-FTRDPLVILDNHNTLLVNDGCHGHTPEAKLRN 279
 QY 203 RLEKHISE---QRAYGCGTSGIEIPVLCVLVNGDPNTLERISRAVEQAAPMLIVGSGGI 259
 DB 280 QLEKISERTSDSNYGG---KIPVCFAGCGRETLKALINTSVKSKIPCVVVEGSGOI 335
 QY 260 ADVLAALVNOPHLVPAKAEKQFKEKFPSS-KHFSMEDIVMTKLLONTSHQHLTYVD 317
 DB 336 ADVIASLVEVEDVLTSSNWKELVFLPRTVSRLEPEEIESITKMKELLESCHLLTYIK 395
 QY 318 FEQSGSEELDTVILKALVAKCKSHQSEPODYDELKELAVAMDVIAKSEIFNGDVEWKS 377

```

Db      396 MEADGEVSSASIALYKAFSTNEDKNNMGOKLLEMMQDLASDEITHRRMS 455
Qy      378 CDLEEVMDALVSNKPEFRLFVNDGADVADFLTGRLOELYSRSRKSLDLLO--R 434
Db      456 ADLOEVMFALLKDRPKFVRLFLGNLNLQKELTMEVLELF-STHFSTLVYRNLIQIANK 514
Qy      435 KOBEARLTLAGIGTQOAREPPAPPAFSLHEVSRVLKDLQACRGFYDDGPRDRAE 494
Db      515 SYNDALLTF-----VKKLVANR-----RSFKEDR----- 540
Qy      495 KCPAKPRFGOKWLLDLNOKSENPMWDLFLMAVLONRHNEMATYFWAMGDEGVAALAAACKI 554
Db      541 ---SSSEDDVDELHDAISLFTTRHPLOALFIMAILQNKELSKVIMWGCTCTLAALGASKL 597
Qy      555 LKEMSHLETAEAAARTREA--KYERLALDLFSECSYNSSEARAFALLVRRNCWSTTCL 612
Db      598 LKTLAKVKNDINNAAGESEELANEYETRAVELFTECYSDEDLAEOLLYVSCAMGSGNCL 657
Qy      613 HLATEADAKAFPAHDGVOAFLTRIMWGDMAAGTPILRLGALFCALVYTNLITFSEBAR 672
Db      658 ELAVEETDQHFIAQPGVQNFSLKQMYGELSRDTKMKIILCFIIPVGGCLVSFRKK-- 715
Qy      673 LRTGLDLQDLSDLTESPLYGLOSRVELEVPAPQDGRGPRAVELLTRMRKFWGAPV 732
Db      716 -----PIDGKK-----LMYYVAFSTSPF 735
Qy      733 TVPLGNVVMYFAFLFTYVLLVDFPRPPQSGPEVTLFVWFVTLVLEIRQGFTEBD 792
Db      736 VVFSNMVVFYIAFLFLFAVLLMDFHSVPH--TPELLIALVFLVFCDEVQWYNGVN 792
Qy      793 THLVKFTLYVGDNNMKCMVAIFLFIYVTCRM--LPSAFAGRTVLAMPVMTLRL 849
Db      793 -----YFTDLNVMWDTLGLFTYAGIVFRLHSSNKSLSYSGVITCLDITITLTL 843
Qy      850 IHIFAIHKOLGPKIIVVERMKDVFFLFFLSVWLVAVGTTQALHPRDGLMEIFRRV 909
Db      844 IHIFTSRNLGPKIIMLOMLDVFFFLFLFAVMVAVFGVARGILRQNEGRMWRIFRSV 903
Qy      910 LTRPVYIQTGQIPLDEIDARVNC-----THPLLE-DSPSCPSLYAMVLLVLLV 960
Db      904 IVEPYLAMEGVPSD-VDSITTYDFSHCTFSGNSKPLCVELDEYNLPR-FPEWITITPLVC 961
Qy      961 TELLVNVLNMLLIMFSYTTPOVGNATMFKPQRNLYIVEYHRPLAPPFILSLH 1020
Db      962 IYMLSTNILLNMLVLMFSGITVGIENNDQWKFQRIYVOEYCNRLNIPPEVFAIF 1021
Qy      1021 SLTLRFVFKAEHKKERLERDLDPDLQKVVTWETVOKENPLSKMEKRRDSEGEVLK 1080
Db      1022 VVVVKKCFCCCKEKTESACCFRMEDEBETLAMEGVMEKNYLVKINTKANDV-AEMKH 1080
Qy      1081 TAHRVDFIKYLGG-LREQEKIK 1103
Db      1081 RFRQDLTKLNDLKLKEIKANKIK 1104

RESULT 15
Q8TDx8      PRELIMINARY;      PRT; 1095 AA.
AC      Q8TDx8;
DT      01-JUN-2002 (T-EMBLrel. 21, Created)
DT      01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT      01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE      LTRPC6.
GN      Homo sapiens (Human).
OS      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      Sano Y., Imamura K., Miyake A., Mochizuki S., Yokoi H., Kitada C.,
      Nozawa K., Matsushima H., Furutachi K.,

```

```

RT      "Molecular cloning of a novel member of LTRP channel family, LTRPC6."
RL      Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB061779; BAB6135.1; -.
DR      InterPro; IPR002111; Cat_channel_TrpL.
DR      InterPro; IPR005821; Ion_trans.
DR      Pfam; PF00520; Ion_trans; 1.
KW      Ionic channel, Transmembrane.
SQ      SEQUENCE 1095 AA; 126634 MW; 3BA3BD4C420361 CRC64;

Query Match      25.6%; Score 1559.5; DB 4; Length 1095;
Best Local Similarity 34.1%; Pred. No. 9.2e-112; Indels 131; Gaps 27;
Matches 377; Conservative 203; Mismatches 394;

Qy      26 GEVNGSGGKRGKGVRRVSGVAPSVLFDLLAEHMLPAPNLVSLVGEOPFAPKSMYR 85
Db      95 GDIGFETLQK-GKIRISCDTDAILVELLQHNHKLTPNLVSVTGAKNFALKPRNR 153
Qy      86 DYLRGLVKAAGSTGAMILTSALRVGLARHGQAVRDSLASTSTKRVVAVGASLGRV 145
Db      154 KIFSR-LIYIAQSGAMILTGTHYGLMKYIGEVRDWTI-SRSSEENIVAIIGIAMGV 211
Qy      146 LHRRLLE--EAOEFPVHIFEDDGSOGPLCSLDSNLSHFTLVPRPGKDGDLTELRL 202
Db      212 SNRDLIRNCABEGYFLAQYIMDD-FTRDPLYLIDNNHTHLVLVNGCHGPTVEAKLN 270
Qy      203 BLEKHISE---ORAGYGTGSIIEIPVLCILVNGDENTLERISRAVEOAAFWLIVGSGI 259
Db      271 QLEKRISETTIDDSNYG---KIPVCPAOGGGETLKAINTSLKNIKPCVNVGSGGI 326
Qy      260 ADVLAALVNPQLVLPVKAQKQKFKPS--KHFSMEDIVRWTKLLQNTSHOHLTYVD 317
Db      327 ADVIASLVEVEDALTSNAVEKELVRFPRTVSRLEPEETESWIKMLKELECSHLITLVK 386
Qy      318 FEQSESELDYIILKALVKACKSHQEPQDYIDELKLVAMRVLIASKEINGVEMKS 377
Db      387 MEADGEVSSASIALYKAFSTSDOKNNMGOKLLEMMQDLADEITINDRRMS 446
Qy      378 CDLEEVMDALVSNKPEFRLFVNDGADVADFLTGRLOELYSRSRKSLDLLO--R 434
Db      447 ADLOEVMFALLKDRPKFVRLFLGNLNLQKELTMEVLELF-SHFSTLVYRNLIQIANK 505
Qy      435 KOBEARLTLAGIGTQOAREPPAPPAFSLHEVSRVLKDLQACRGFYDDGPRG-DRRA 493
Db      506 SYNDALLTF-----VKKLVANR-----RGFRKEDHNGDEMDI 539
Qy      494 KCPAKPRFGOKWLLDLNOKSENPMWDLFLMAVLONRHNEMATYFWAMGDEGVAALAAACK 553
Db      540 E-----LHDVSPITRHPLOALFIMAILQNKELSKVIMWGCTCTLAALGASK 587
Qy      554 LKEMSHLETAEAAARTREA--KYERLALDLFSECSYNSSEARAFALLVRRNCWSTTCL 611
Db      588 LKTLAKVKNDINNAAGESEELANEYETRAVELFTECYSDEDLAEOLLYVSCAMGSGN 647
Qy      612 HLATEADAKAFPAHDGVOAFLTRIMWGDMAAGTPILRLGALFCALVYTNLITFSEBAR 671
Db      648 ELAVEATDQHFIAQPGVQNFSLKQMYGELSRDTKMKIILCFIIPVGGCFVSFRKK- 706
Qy      672 PLRTGLDLQDLSDLTESPLYGLOSRVELEVPAPQDGRGPRAVELLTRMRKFWGAP 731
Db      707 -----PVDKHK-----LMYYVAFSTSPF 725
Qy      732 TVVPLGNVVMYFAFLFTYVLLVDFPRPPQSGPEVTLFVWFVTLVLEIRQGFTEBD 791
Db      726 VVFSNMVVFYIAFLFLFAVLLMDFHSVPH--PPELVLYSLVFLFCDEVQWYNGVN 782
Qy      792 DTHLVKFTLYVGDNNMKCMVAIFLFIYVTCRM--LPSAFAGRTVLAMPVMTLRL 848
Db      783 N-----YFTDLNVMWDTLGLFTYAGIVFRLHSSNKSLSYSGRVFCLDYIIFTLR 833
Qy      849 LHIHFAIHKOLGPKIIVVERMKDVFFLFFLSVWLVAVGTTQALHPRDGLMEIFRR 908
Db      834 LHIHFTSRNLGPKIIMLOMLDVFFFLFLFAVMVAVFGVARGILRQNEGRMWRIFRS 893

```


THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)